

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2000, 19:36:16 ; Search time 3853.81 Seconds
(without alignments)
199.863 Million cell updates/sec

Title: US-09-183-789-1
Perfect score: 204
Sequence: 1 gatcgttactcctcctcaag.....gacactgtactgtttcgtgc 204

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database: EST.*

Word size: 0

Number of hits that pass the threshold: 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
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68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
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96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
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101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	184.2	90.3	515	74	AA197564	AA197564 xm44d05.x
2	179.2	87.8	510	63	AAW004014	AAW004014 wg94h07.x
3	174.2	85.4	505	49	AA1624830	AA1624830 ts71f12.x
4	110	53.9	330	29	AA155054	AA155054 mr91b11.r
5	108.4	53.1	425	42	AA1654710	AA1654710 wb49c06.x
6	107.6	52.7	336	42	AA1085076	AA1085076 ow88h01.s
7	99	48.5	466	29	AA170068	AA170068 ms44c07.f

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      8 76.4 37.5 459 26 W86797
      9 70 34.3 551 34 AA496651
     10 61.8 30.3 433 69 AM102885
     11 61.6 30.2 454 38 AA757285
     12 61.6 30.2 427 39 AA865734
     13 61.6 30.2 418 45 AI355317
     14 58.4 28.6 263 29 AA189462
     15 58.4 28.6 440 30 AA203802
     16 47.6 23.3 443 24 H83744
     17 46 22.5 322 33 AA448534
     18 42 20.6 715 62 AI921056
     19 41.8 20.5 761 103 AQ487699
     20 41.2 20.2 502 44 AI344063
     21 39.6 19.4 486 48 AI581344
     22 39.2 19.2 531 41 AI1015911
     23 39 19.1 238 70 AV253285
     24 38.6 18.9 663 99 AQ249576
     25 38.2 18.7 437 40 C90865
     26 37.4 18.3 217 41 AU011742
     27 37 18.1 357 102 AQ415510
     28 36.8 18.0 1101 79 C9S008X5
     29 36.8 18.0 896 81 BI0661
     30 36.6 17.9 319 40 C92584
     31 36.6 17.9 565 40 C93739
     32 36.4 17.8 585 102 AQ384109
     33 36.2 17.7 1101 79 C9S008G7
     34 36.2 17.7 1117 79 C9S00Z25
     35 36 17.6 410 100 AQ295460
     36 35.8 17.5 430 22 AI5281
     37 35.8 17.5 486 61 AL041544
     38 35.8 17.5 1101 80 C9S017X
     39 35.6 17.5 383 23 H59015
     40 35.6 17.5 566 99 AQ238014
     41 35.4 17.4 559 40 C89995
     42 35.4 17.4 240 51 AU073371
     43 35.4 17.4 240 51 AU073690
     44 35.2 17.3 655 79 AG020469
     45 35.2 17.3 1101 79 C9S006EA

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ALIGNMENTS

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RESULT 1
LOCUS AM197564 515 bp mRNA EST 29-NOV-1999
DEFINITION xm44605.x1 NCI-CGAP_GC6 Homo sapiens cDNA clone IMAGE:2687049 3'
Similar to TR:061204 061204 NOTCH2-LIKE ;, mRNA sequence.
ACCESSION AM197564
VERSION AM197564.1 GI:6476794
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL On Jul 8, 1999 this sequence version replaced gi:5422498.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.11nl.gov/bbrp/image/image.html

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FEATURES
source Seq primer: -40UP from Gibco
High quality sequence stop: 452.
Location/Qualifiers
1..515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2687049"
/tissue_type="NCI-CGAP_GC6"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker. Plasmid DNA from the normalized library
NCI-CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clonoids 1257096-1258631,
1469064-1470983, and 1475592-1476743)." Subtraction by
Bento Soares and M. Fatima Bonaldo.

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BASE COUNT 131 a 105 c 83 g 196 t
ORIGIN
Query Match 90.3%; Score 184.2; DB 74; Length 515;
Best Local Similarity 98.0%; Pred. No. 7.4e-34;
Matches 197; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY 1 gatctgttaccctcttcaagaaatgaatcttccataatttgcacaccttga 60
DB 315 GATCCTTGTACTCTTCAAGCAAAATGAAATCTTTCATATATTTGCCAACCTTGA 374
QY 61 actcttcatlaattgatattatatacatcalttaattcttgcacatgcagagat 120
DB 375 ACTTCTTTCATTAATTCATATTTATATCATATTAATTTCTTCCATGCGACGAGAT 434
QY 121 attgttgtratttgcacagttt-cacggaacattctgaactgtgggtcagct 179
DB 435 ATTGTGtGtATTtGGcACAGtTTCcACAAAGAcATTACTGtGGtGtCACT 494
QY 180 gcagagacacgttagttttg 200
DB 495 GCAGAGACACGTGAGTTTtTG 515

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RESULT 2
LOCUS AM004014 510 bp mRNA EST 08-SEP-1999
DEFINITION wg94407.x1 NCI-CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479741 3'
Similar to TR:061204 061204 NOTCH2-LIKE ;, mRNA sequence.
ACCESSION AM004014
VERSION AM004014.1 GI:5850930
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL On Jun 5, 1998 this sequence version replaced gi:3189727.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/db/ncbi/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 454.

FEATURES

source
1. 510
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2479741"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 131 a 105 c 82 g 192 t

ORIGIN

Query Match 87.8% Score 179.2; DB 63; Length 510;
Best Local Similarity 98.0%; Pred. No. 1.1e-32;
Matches 192; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 gatgtgtgacctcttcaagaacaaatgaaattcttcataatttgcacaaacctcga 60
|||||
Db 315 GATCCTTGTAACCTTTGACGAAATGAAATTTCTTCATATATTTGCCCAACCTTGA 374
|||
OY 61 actcttcaatgatatattatcatcattatcttctgcacgagcagagat 120
|||||
Db 375 ACTCTTTCATATATGATATTTATCATCATTAATTTCTTGCATGCGAGAGAT 434
|||||
OY 121 attgtgtgatttggcacagttt-caccgaagacattcgttaactggtggtcagct 179
|||||
Db 435 ATTGTGTTGATTTGGCACAGTTTCCACCAAGACATTAAGTGTGAGTGTGACCT 494
|||||
OY 180 gcaagagacactgtagt 195
|||||
Db 495 GCAGAGACACTGTAGT 510

LOCUS 3
A1624830

DEFINITION A1624830 505 bp mRNA EST 22-APR-1999
ts71112.x1 NCI_CGAP_Homo sapiens cDNA clone IMAGE:2236751 3'
similar to TR:061204 Q61204 NOTCH2-Like ;, mRNA sequence.

ACCESSION A1624830
VERSION A1624830.1 GI:4649761
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3187074.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.

JOURNAL
COMMENT

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/db/ncbi/image/image.html

Seq primer: -40UP from Gibco
High quality sequence stop: 452.

FEATURES

source
1. 505
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2236751"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 130 a 105 c 80 g 190 t

ORIGIN

Query Match 85.4% Score 174.2; DB 49; Length 505;
Best Local Similarity 97.9%; Pred. No. 1.6e-31;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 gatgtgtgacctcttcaagaacaaatgaaattcttcataatttgcacaaacctcga 60
|||||
Db 315 GATCCTTGTAACCTTTGACGAAATGAAATTTCTTCATATATTTGCCCAACCTTGA 374
|||
OY 61 actcttcaatgatatattatcatcattatcttctgcacgagcagagat 120
|||||
Db 375 ACTCTTTCATATATGATATTTATCATCATTAATTTCTTGCATGCGAGAGAT 434
|||||
OY 121 attgtgtgatttggcacagttt-caccgaagacattcgttaactggtggtcagct 179
|||||
Db 435 ATTGTGTTGATTTGGCACAGTTTCCACCAAGACATTAAGTGTGAGTGTGACCT 494
|||||
OY 180 gcaagagacact 190
|||||
Db 495 GCAGAGACACT 505

RESULT 4
A155054/c 330 bp mRNA EST 11-FEB-1997
LOCUS A155054
DEFINITION A155054 330 bp mRNA EST 11-FEB-1997
mr91d11.r1 Stragene mouse embryonic carcinoma (#937317) Mus
musculus cDNA clone IMAGE:604797 5' similar to TR:G1336628 G1336628
EST REPEAT TRANSMEMBRANE PROTEIN ;, mRNA sequence.

ACCESSION A155054
VERSION A155054.1 GI:1726674
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 330)

AUTHORS

Maria M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisels S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Stepice M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Wilson R. and
Waterston R.

The WashU-HMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1292301.
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project

JOURNAL
COMMENT


```

/organism="Homo sapiens"
/db_xref="GDB:1325310"
/db_xref="taxon:9606"
/clone="IMAGE:416840"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT      147 a      89 c      63 g      160 t

Query Match
Best Local Similarity 84.3%; Score 76.4; DB 26; Length 459;
Matches 86; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1 gatcgtgtacctcttcaagcaaaatgaaatcttcataatttgcacaaaccttga 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 358 GGTCTTCACACTTCTTCAAGCAAAATGAAATCTTTCATATTTCGACCAACTTCGA 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 61 actcttcataattgataatttatacattcaatttc 102
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 418 ACTCTCTCATTAATTGATGATTATATCATGCAATTCGATTC 459

RESULT 9
AA496651/c
LOCUS      551 bp      mRNA      EST      12-AUG-1997
DEFINITION zvf7f09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:755849 5' similar to TR:G1336628 G1336628 EGF REPEAT
            TRANSMEMBRANE PROTEIN.; mRNA sequence.
ACCESSION  AA496651
VERSION     AA496651.1 GI:2229972
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kuwaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,D.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            WashU-Merck EST Project 1997
            Unpublished (1997)
TITLE       On Jan 25, 1995 this sequence version replaced gi:637829.
JOURNAL     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m3 rev2 Et from Amersham
            High quality sequence stop: 508.
FEATURES
            Location/Qualifiers
            1..551
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:755849"
            /clone_lib="Soares ovary tumor NbHOT"

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```

/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTAAGTGGAGCGCCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT      180 a      89 c      121 g      161 t

Query Match
Best Local Similarity 84.3%; Score 70; DB 34; Length 551;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 gatcgtgtacctcttcaagcaaaatgaaatcttcataatttgcacaaaccttga 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 118 GGTCTTCACACTTCTTCAAGCAAAATGAAATCTTTCATATTTCGACCAACTTCGA 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 61 actcttcataattgataatttatacattcaatttc 86
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 58 ACTCTCTCATTAATTGATGATTATATCATGCAATTCGATTC 63

RESULT 10
AM102885
LOCUS      433 bp      mRNA      EST      19-OCT-1999
DEFINITION x439g11.x1 NCI-CGAP-Ov23 Homo sapiens cDNA clone IMAGE:2596196 3'
            similar to TR:Q61204 Q61204 NOTCH2-LIKE.; mRNA sequence.
ACCESSION  AM102885
VERSION     AM102885.1 GI:6073498
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 433)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            On Jun 22, 1998 this sequence version replaced gi:3246955.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www-bio.llnl.gov/bdrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 358.
FEATURES
            Location/Qualifiers
            1..433
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2596196"
            /clone_lib="NCI-CGAP-Ov23"
            /tissue_type="tumor; 5 pooled (see description)"
            /lab_host="DH10B"
            /notes="Organ: ovary; Vector: PCWV-SPOF6; Site_1: SalI;
            Site_2: NotI. Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.35 kb. Tumor types include: mixed

```


RESULT 8

LOCUS W86797 459 bp mRNA EST 01-JUL-1996
DEFINITION zh64c05.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:416840 3', mRNA sequence.
ACCESSION W86797
VERSION W86797.1 GI:1400525
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 459)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasik,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On May 16, 1995 this sequence version replaced gi:808442.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 361.
Location/Qualifiers
1. .459

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/organism="Homo sapiens"
/db_xref="GDB:1325310"
/db_xref="taxon:9605"
/clone="IMAGE:416840"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library." 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AACTGGAAGAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

BASE COUNT	147 a	89 c	63 g	160 t
ORIGIN				

Query Match 37.5%; Score 76.4; DB 26; Length 459;
Best Local Similarity 84.3%; Pred. No. 1.2e-08;
Matches 86; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 gatcgttgtagacctcttcaagcaaaatgaaaattctttcataattttgccaaaccttcga 60
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Db 358 GGTCCCTTGCACCTCTCTCAAGCAAAATGAAAAATTCTTCATATTTTCGACCAAACCTTCGA 417

Qy 61 actctcttttcattaattgatattttatatcatcattaattttc 102
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Db 418 ACTTCCTTCATTAAATGGATGGITTATATCAGCATTTGGATTCC 459

RESULT 9
AA496651/C
LOCUS

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 13:21:14 ; Search time 172.6 Seconds
(without alignments)
1708.448 Million cell updates/sec

Title: US-09-183-789-43

Perfect score: 2463
Sequence: 1 gcttggtaccgagctcgat.....aaaaaaaaaaaaaaaaaaaaa 2463

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 214294 seqs, 59861574 residues

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2.6/ptodata/1/ina/5C.COMB.seq:*
- 4: /cgn2.6/ptodata/1/ina/5D.COMB.seq:*
- 5: /cgn2.6/ptodata/1/ina/6.COMB.seq:*
- 6: /cgn2.6/ptodata/1/ina/PCITUS9.COMB.seq:*
- 7: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60.2	2.4	19124	4	US-08-487-826B-13 Sequence 13, Appl
2	56	2.3	665	4	US-08-883-795A-36 Sequence 36, Appl
3	54	2.2	19124	4	US-08-487-826B-13 Sequence 13, Appl
4	53.8	2.2	7218	1	US-08-232-463-14 Sequence 14, Appl
5	52.4	2.1	4525	1	US-08-613-861-2 Sequence 2, Appl
6	51.6	2.1	1123	1	US-08-458-023B-3 Sequence 3, Appl
7	50.6	2.1	5852	1	US-07-867-106-2 Sequence 2, Appl
8	50.4	2.0	1511	1	US-07-991-867B-8 Sequence 8, Appl
9	50.4	2.0	1511	2	US-08-107-755A-8 Sequence 8, Appl
10	50.4	2.0	1511	2	US-08-544-332-8 Sequence 8, Appl
11	50.2	2.0	9837	2	US-08-832-883-68 Sequence 68, Appl
12	50.2	2.0	9837	3	US-08-832-877-68 Sequence 68, Appl
13	50	2.0	3984	1	US-08-040-753-1 Sequence 1, Appl
14	50	2.0	4059	3	US-08-252-493C-4 Sequence 4, Appl
15	50	2.0	4059	6	PCT-US95-07554-4 Sequence 4, Appl
16	50	2.0	4059	6	PCT-US95-05611A-11 Sequence 11, Appl
17	50	2.0	6420	1	US-08-374-483-1 Sequence 1, Appl
18	50	2.0	9592	1	US-08-393-734-3 Sequence 3, Appl
19	48.6	2.0	665	4	US-08-883-795A-36 Sequence 36, Appl
20	48.4	2.0	1982	4	US-08-900-148-1 Sequence 1, Appl
21	48.2	2.0	660	1	US-07-991-867B-32 Sequence 32, Appl
22	48.2	2.0	660	2	US-08-107-755A-32 Sequence 32, Appl
23	48.2	2.0	660	4	US-08-544-332-32 Sequence 32, Appl
24	48	1.9	404	4	US-08-594-031-154 Sequence 154, Appl
25	47.8	1.9	1700	4	US-08-839-581A-1 Sequence 1, Appl
26	47.8	1.9	115	3	US-08-454-557C-75 Sequence 75, Appl
27	47.8	1.9	115	4	US-08-340-426D-75 Sequence 75, Appl

28	47.8	1.9	115	4	US-08-450-673C-75 Sequence 75, Appl
29	47.8	1.9	115	6	PCT-US95-1711A-75 Sequence 2, Appl
30	47.8	1.9	5852	4	US-07-867-106-2 Sequence 1, Appl
31	47.6	1.9	6243	4	US-09-056-075-1 Sequence 14, Appl
32	47.2	1.9	2447	4	US-09-014-969-14 Sequence 4, Appl
33	47	1.9	4098	4	US-08-605-106-4 Sequence 13, Appl
34	46.6	1.9	1672	1	US-08-172-331B-13 Sequence 76, Appl
35	46.2	1.9	120	3	US-08-454-557C-76 Sequence 76, Appl
36	46.2	1.9	120	4	US-08-340-426D-76 Sequence 76, Appl
37	46.2	1.9	120	6	US-08-450-673C-76 Sequence 76, Appl
38	46.2	1.9	120	6	PCT-US95-1711A-76 Sequence 76, Appl
39	45.8	1.9	1629	6	PCT-US91-02560-3 Sequence 3, Appl
40	45.8	1.9	4673	1	US-07-636-431-1 Sequence 1, Appl
41	45.8	1.9	4673	6	PCT-US92-00018-1 Sequence 1, Appl
42	45.6	1.9	240	1	US-08-628-417-6 Sequence 6, Appl
43	45.6	1.9	642	2	US-08-764-100-13 Sequence 13, Appl
44	45.6	1.9	643	2	US-08-764-100-7 Sequence 7, Appl
45	45.6	1.9	2993	2	US-08-764-100-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-487-826B-13/C
Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chinitz, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487, 826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001Cp1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13
Query Match 2.4%; Score 60.2; DB 4; Length 19124;

Best Local Similarity 46.9%; Pred. No. 0.00019;
Matches 222; Conservative 0; Mismatches 248; Indels 3; Gaps 1;

QY 1928 aatttatttacttgaaatttgaagaacgagcgtgtaaggagtaactaaactaattcgt 1987
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Db 15966 AATTATTATTATTATTATTATTAAATTTTATTATTATTATTATTATTATTAAAT 15907
QY 1988 tcttaaaagaatttattcgcgaatgtagagtcgagatattagctaaatgaatcgt 2047
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Db 15906 TTTTATTATTATTATTATTATTAAATTTTATTATTATTATTATTATTATTAAAT 15847
QY 2048 tgttggggttactctctgttcttcaagtaagaatgtagaagaatttgaagaaccaa 2107
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Db 15846 AATTTTATTATTATTATTATTATTATTAAATTTTATTATTATTATTATTATTATTAA 15787
QY 2108 tgaataattctcagctgcgcaaatgtagcactcttataattcttcttccacttga 2167
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Db 15786 TTTTATTATTACATTTTTAAATTTTATTATTATTATTATGATATATATTATTATTAA 15727
QY 15768 tcttataatataatgtagtgcgtttaaataatgtagatatttcaaga---ttcgtc 2224
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Db 15726 AATTTTATTCTTTTATTGTTTATGATATATATTTTTATTGTTTTT 15667
QY 2225 ttgccttaaatattatcccaattgccttcagtcattcatttgcgtagatatttt 2284
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Db 15666 TTTTCTTCTTTGTTTATTATTATTATTATATCATTTTATTATTAAATTTT 15607
QY 2285 gaattcagtttccataatcattagaagatgagatataaaagaatataaggcaatca 2344
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Db 15606 TTAATTTTATTATTATATCTTTTCAATTTTATTATGCAATAATTTATTATTAT 15547
QY 2345 tatattcaatcaaaagatatatttagcaacgctatgcttccgtcgtt 2397
|||||
Db 15546 AATTTTATTATTATTATAAAAAATTTTCTCTTTTATTATTATTATT 15494

RESULT 2

US-08-883-795A-36/C
Sequence 36, Application US/08883795A
Patent No. 5985607

GENERAL INFORMATION:

APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA

ORIGINAL SOURCE:
ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
CLONE: Rh 32

US-08-883-795A-36

Query Match

2.3%; Score 56; DB 4; Length 665;
Best Local Similarity 46.4%; Pred. No. 0.00065;
Matches 217; Conservative 0; Mismatches 250; Indels 1; Gaps 1;

QY 1629 ttaagaanaaccaaagttccgtcgtctgaagataactgaattaaatttgtaata 1688
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Db 480 TGTAAATATTAATACCTTTAATAAATGTAAATATTAATAATATGTAATTATAAACATT 421
QY 1689 ctgttggaacttgataaagaagccatctcgagaatgtagctaccacaagaagctc 1748
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Db 420 ATTATATAAATATGTAAATTATAACATTTTAATTATTAATAATATGTAATTATAAACATT 361
QY 1749 gtcatataaggtatttccaataaacacattatgtaaggaagtcgcaaatcattatc 1808
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Db 360 ATTATATAAATATGTAAATTATAAACATTTTAATTATTAATAATATGTAATTATAAACATT 301
QY 1809 aatgtgagactcttagaactaactagatcgaattgagagacataacaatagatgat 1868
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Db 300 ATTATATAAATATTAATTAATAAACATTTTAATTATTAATAATATTTAATAATATT 241
QY 1869 accaataacttttgtttttaaacaagctatccaagaagctatcagatgctgctaa 1928
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Db 240 ATTATATAAATATTAATTAATAAATATTTAATTATAAATATTTAATAATATT 181
QY 1929 atttattacttgaaatttgaagaactgagctgtgttaaggataaactaaattctgct 1988
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Db 180 ATTATATAAATATTTAATTATAAATATTTTAAT--TATAAATATTATAATATT 122
QY 1989 cttaaaagaatttattcgcgaatgtagcaagtcctgagatattagctaaatgaatcgt 2048
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Db 121 AATTATTAATAATATTTAATTATAAATATTTAATTATAAATATTTAATAATATT 62
QY 2049 gtttggggttactcttctgttcttaagataagaatgtagaagaattc 2096
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Db 61 AATTATTAATAATTTTAATTATAAATATTTAATTATAAACAAT 14

RESULT 3

US-08-487-826B-13
Sequence 13, Application US/08487826B
Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487, 826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israel, Ben, Ned
 REGISTRATION NUMBER: 29, 655
 REFERENCE/DOCKET NUMBER: NH121.001CPT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ. ID NO.: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19124 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 -08-487-826B-13

Query Match	2.28	Score 54	DB 4	Length 19124
Best Local Similarity	51.08	Pred	No. 0.0043	
Matches 153	Conservative 0	Mismatches 145	Indels 2	Gaps 1

[illegible]

R 234
 US 06-232-463-14/c
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOMLOPX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F15
US-08-232-463-14

Query Match	2.2%	Score	53.8	DB	1	Length	7218
Best Local Similarity	4.0%	Pred.	No. 0.0037				
Matches	16	Conservative	222	Mismatches	159	Indels	0
						Gaps	0

[illegible]

RESULT 5
US-08-613-861-2
; Sequence 2, Application US/08613861
; Patent No. 5843770
; GENERAL INFORMATION:
; APPLICANT: Ill, Charles R. et al.
; TITLE OF INVENTION: Antisense constructs Directed Against Viral Post-Transcript
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,861
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/111,111
FILING DATE: 12-DEC-1909
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Name Init
REGISTRATION NUMBER: 000000
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4525 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-613-861-2

Query Match 2.1% Score 52.4; DB 3; Length 4525;
Best Local Similarity 79.5%; Pred. No. 0.0065;
Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 gcttggtacgagctcgatccatcagtaacgagccgagctgctggaaggagcgca 60
|||||
DB 3090 gcttggtacgagctcgatccatcagtaacgagccgagctgctggaaggagcgca 3149
|||||

QY 61 ccggcgctgcagacagcct 78
|||||
DB 3150 tccgctcgttcacattgct 3167
|||||

RESULT 6
US-08-458-023B-3
Sequence 3, Application US/08458023B
Patent No. 5667990
GENERAL INFORMATION:
APPLICANT: Berkta, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boomlathnan, Katuppan C.
TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4086.010-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Humicola insolens
INDIVIDUAL ISOLATE: DSM 6995
FEATURE:
NAME/KEY: CDS
LOCATION: 126..806
US-08-458-023B-3

Query Match 2.1% Score 51.6; DB 1; Length 1123;
Best Local Similarity 93.1%; Pred. No. 0.0067;
Matches 54; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gcttggtacgagctcgatccatcagtaacgagccgagctgctggaaggagcgca 58
|||||
DB 28 gcttggtacgagctcgatccatcagtaacgagccgagctgctggaaggagcgca 85
|||||

RESULT 7
US-07-867-106-2/c
Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single

Db 883 ATTAATAATATATCAGAAATTAGTAATCAATTTGATATATTTTTCATTGA 824

Qy 2290 ctatgttt 2297

Db 823 TTAATTTT 816

RESULT 9

US-08-107-755A-8/c

Sequence 8, Application US/08107755A

Patent No. 5721352

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Hall, Richard L.

APPLICANT: Gruidl, Michael E.

TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: U.S.A.

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,755A

FILING DATE: 19-AUG-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,658

FILING DATE: 30-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/657,584

FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UFI14.C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1511 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Amsacta moorei entemopoxvirus

FEATURE:

NAME/KEY: CDS

LOCATION: complement (18..218)

FEATURE:

NAME/KEY: CDS

LOCATION: complement (234..782)

FEATURE:

NAME/KEY: CDS

LOCATION: 852..1511

US-08-107-755A-8

Query Match 2.0%; Score 50.4; DB 2; Length 1511;

Best Local Similarity 46.5%; Pred. No. 0.013;

Matches 199; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

Qy 1873 aatactttgttttaacacagcctatccagtaagcctatcgtatgctgctctaaattt 1932

Db 1243 ATTAATTTTTTAAATTACTAAATTAATTAATAAATTAATGCTAATTATATACANGAT 1184

Qy 1933 tattacttgaattttgaaactgacgtgctgtagggatlaaactataactctgtctta 1992

Db 1183 TCACATTTTAAATAATTCATATGAAATGTGGTAGTATAATATTAATTAATTCCTATTTTG 1124

Qy 1993 aaagaattcatctgcaatgctgcaagttctggatattagctcaatgaattgcttt 2032

Db 1123 TTATAGATATATCTTAATAATTAATTAATTTTAAATTTGTTAAATAATTAATA 1064

Qy 2053 ggggttactctcttcttcttaagataagaaatgtaagaatttgaagaactcaatg 2109

Db 1063 ATATTTAAATTTGAAATATATAAATCTTTTAATTAATTTTGTGAAATTAATTTAAATAATA 1004

Qy 2110 aataatctcagctgccaagtgtgcacctcttataatcttctccactttgctc 2169

Db 1003 TTATCATATATATATATATATATGCAATCTCTTAATTAATTAATTTTAAATATATATA 944

Qy 2170 tattatataatgtagtcttttaaaatgctgataatttcagacttgcttgc 2229

Db 943 TTAATTAACATTAATCTCTGTTATTAATTAATTTTAAATTAATTAATTAATTAATTT 884

Qy 2230 cttaatatatacccaattctcagtcacatcttctgctcagatatataattgaatt 2289

Db 883 ATTAATAATATATCAGAAATTAGTAATCAATTTGATATATTTTTCATTGA 824

Qy 2290 ctatgttt 2297

Db 823 TTAATTTT 816

RESULT 10

US-08-544-332-8/c

Sequence 8, Application US/08544332

Patent No. 5935777

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Hall, Richard L.

APPLICANT: Gruidl, Michael E.

TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Gerard H. Bencen

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/544,332

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,867

FILING DATE: 07-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/107,755

FILING DATE: 19-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO 92/14818

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,685

FILING DATE: 30-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/657,584

FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:

```

1 NUMBER OF SEQUENCES: 115
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
4 STREET: Suite 1800 Two Penn Center Plaza
5 CITY: Philadelphia
6 STATE: PA
7 COUNTRY: USA
8 ZIP: 19102
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patentn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/832.883
17 FILING DATE:
18 CLASSIFICATION: 435
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Monaco, Daniel A
21 REGISTRATION NUMBER: 30,480
22 REFERENCE/DOCKET NUMBER: 8321-13 US1
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (215) 568-8383
25 TELEFAX: (215) 568-5549
26 INFORMATION FOR SEQ ID NO: 68:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 9837 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: double
31 TOPOLOGY: linear
32 MOLECULE TYPE: DNA (genomic)
33 US-08-832-883-68
34
35 Query Match 2.0%: Score 50.2; DB 2; Length 9837;
36 Best Local Similarity 81.7%: Pred. No. 0.024;
37 Matches 58; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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39 QY 1 gcttgtagcagagctcgagatccactagtaacggccgacgtgtctggaaggagccca 60
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41 Db 7173 gcttgtagcagagctcgagatccactagtaacggccgacgtgtctggaaggagccca 60
42 |||||||
43 QY 61 ccggagcgctga 71
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45 Db 7233 AGTAGGCGGA 7243
46
47 RESULT 12
48 US-08-832-877-68
49 : Sequence 68, Application US/08832877
50 : Patent No. 5840506
51 : GENERAL INFORMATION:
52 APPLICANT: Giordano, Antonio
53 TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
54 TITLE OF INVENTION: CANCER
55 NUMBER OF SEQUENCES: 116
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
58 STREET: Suite 1800 Two Penn Center Plaza
59 CITY: Philadelphia
60 STATE: PA
61 COUNTRY: USA
62 ZIP: 19102
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible
66 OPERATING SYSTEM: PC-DOS/MS-DOS
67 SOFTWARE: Patentn Release #1.0, Version #1.30
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/08/832.877
70 FILING DATE:
71 CLASSIFICATION: 436
72 ATTORNEY/AGENT INFORMATION:

```

NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-877-68

Query Match 2.0%; Score 50.2; DB 3; Length 9837;
Best Local Similarity 81.7%; Pred. No. 0.024;
Matches 58; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Oy 61 ccggagcgctga 71
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Db 7233 AGTAGGCGGA 7243

RESULT 13
US-08-040-753-1
Sequence 1, Application US/08040753
Patent No. 5464745
GENERAL INFORMATION:
APPLICANT: Mierendorf, Robert
APPLICANT: Garber, Richard
APPLICANT: No. 5464745y, Robert
APPLICANT: Hammer, Beth
TITLE OF INVENTION: Protein Ligand Binding
TITLE OF INVENTION: Region Mapping System
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: 1 South Pinckney St., Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,753
FILING DATE: 19930331
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 70-399-9001-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3984 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTOPE-1b(+)
FEATURE:
NAME/KEY: Promoter
LOCATION: 67..85
OTHER INFORMATION: /function= "T7 Promoter"
FEATURE:
NAME/KEY: RBS
LOCATION: 134..139
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1092
OTHER INFORMATION: /product= "5' end of T7 gene 10
OTHER INFORMATION: fusion protein"/note= "this coding region is interrupted
OTHER INFORMATION: during cloning by insertion of putative epitope encoding
OTHER INFORMATION: DNA."
US-08-040-753-1

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcttgtagcgaagctcgagatccactagtaacgcccagctgtctggaag 50
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Db 938 GCTTGTCACGAGCTCGGATCCACTAGTAACGCCGCCAGTGTGTA 987

RESULT 14
US-08-252-493C-4
Sequence 4, Application US/08252493C
Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid

DESCRIPTION: Apex-1 Eukaryotic
 DESCRIPTION: Expression Vector
 US-08-252-493C-4

Query Match 2.0%: Score 50; DB 3; Length 4059;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1027 GCTTGATCCGAGCTCGATCCACTAGTAACGCCGCCAGTGTGCTGAA 1076

RESULT 15
 PCT-US95-07554-4
 Sequence: Application PC/TUS9507554
 GENERAL INFORMATION:

APPLICANT: Sandrin, Mauro S.
 APPLICANT: Fodor, William L.
 APPLICANT: Rother, Russell P.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: McKenzie, Ian F. C.
 TITLE OF INVENTION: Methods for Reducing
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Maurice M. Klee
 STREET: 1951 Burr Street
 CITY: Fairfield
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06430

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 750 Kb storage
 COMPUTER: Dell 486/50
 OPERATING SYSTEM: DOS 6.2
 SOFTWARE: WordPerfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07554
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/260,201
 FILING DATE: June 15, 1994
 CLASSIFICATION:
 APPLICATION NUMBER: 08/278,282
 FILING DATE: July 21, 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Klee, Maurice M.
 REGISTRATION NUMBER: 30,399
 REFERENCE/DOCKET NUMBER: ALX-144.1PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 255-1400
 TELEFAX: (203) 254-1101
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4059 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: Circular
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: Apex-1 Eukaryotic
 DESCRIPTION:
 ANTI-SENSE: NO
 PCT-US95-07554-4

Query Match 2.0%: Score 50; DB 6; Length 4059;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1027 GCTTGATCCGAGCTCGATCCACTAGTAACGCCGCCAGTGTGCTGAA 1076

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 Job time: 8171 sec

Fri Mar 24 13:38:33 2000

us-09-183-789-43.rni

Page 10

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GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2000, 21:51:58 ; Search time 3853.81 Seconds
(without alignments)
2413.056 Million cell updates/sec

Title: US-09-183-789-43

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105: gb_est45:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	519.2	21.1	559	41	A1052728	A1052728 oz27b05.x
2	504.2	20.5	639	100	A0280053	A0280053 CITBI-E1-
3	501.2	20.3	517	38	AA807217	AA807217 oc35g09.s
4	499.8	20.3	503	61	AT810084	AT810084 wf65c09.x
5	362.6	14.7	692	35	AA545060	AA545060 v91a10.s
6	356.8	14.5	456	30	AA213817	AA213817 zt91d11.s
7	326	13.2	328	38	AA756999	AA756999 ah54b09.s

C	8	325	13.2	482	39	AA825936
	9	312.4	12.7	698	102	AQ376588
	10	271	11.0	387	33	AA420348
	11	269.4	10.9	367	33	AA907054
C	12	258.2	10.5	378	100	AQ261251
	13	206.2	8.4	496	87	AQ791096
	14	185	7.5	501	30	AA240712
	15	174.2	7.1	564	102	AA415970
	16	173.4	7.0	654	70	AM153497
	17	166.4	6.8	405	36	AA609375
	18	161.8	6.6	656	104	AQ534381
	19	138	5.6	612	69	AM133819
C	20	131	5.3	620	70	AM154095
	21	130.2	5.3	185	30	AA213896
	22	110.8	4.5	327	64	AL118219
	23	106.4	4.3	557	22	R78674
	24	100.8	4.1	259	30	AA254513
C	25	96.8	3.9	1101	79	CNS00EVL
	26	94.2	3.8	1101	80	CNS0145U
C	27	86.2	3.5	1101	79	CNS0039C
	28	84	3.4	1101	79	CNS0039C
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	30	80	3.2	1101	79	CNS0039C
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	42	72.6	2.9	1101	79	CNS0021J
C	43	72.2	2.9	1043	80	CNS0145P
	44	72	2.9	1225	80	CNS0161D
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ALIGNMENTS

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AQ376588	RPCR-11-1
AA420348	v01g02.s
AA907054	cm10g08.s
AQ261251	CITBI-EI-
AQ791096	HS-2189.B
AA240712	mv30b11.r
AA415970	RPCR-11-2
AM153497	f122d05.y
AA609375	zu/1e10.s
AQ534381	RPCR-11-3
AM133819	f112c01.y
AM154095	f122d05.x
AA213896	z91d11.f
AL118219	f6c10b03
R78674	y174d03.r1
AA254513	va17c12.r
AL069706	prosoph11
AL103740	prosoph11
AL063921	prosoph11
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RESULT 1
LOCUS A1052728 559 bp mRNA EST 01-OCT-1998
DEFINITION o27b05.x1 Soares.totat.fetus.Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1676529 3', mRNA sequence.
VERSION A1052728
KEYWORDS A1052728.1 GI:3308719
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 559)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2152886.
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Insert Length: 2396 Std Error: 0.00
Seq Primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 492.
Location/Qualifiers
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/db_xref="taxon:9606"

FEATURES
source

BASE COUNT 189 a 113 c 123 g 133 t 1 others
ORIGIN
Query Match 21.8%; Score 519.2; DB 41; Length 559;
Best Local Similarity 99.28; Pred.No. 1.1e-87;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: PT7T3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer (5'
GTGTACCAATCTGAGGTGGGCGGCTTAATTTTGTGTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and W. Fatima Bonaldo."

QY 51 aggaagccacacggcgctgacagacctatgagagcaggggtgtgctccgggacctta 110
|||||
Db 35 ATGACGCCACCGGGCGCTGACAGACCTATGAGAGTCAGGGTGTGCTCCGGGCTTA 94
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QY 111 tcgggcccacacgaagtgtggaatggaatcacacatcttcgagcaggaatgacctaa 170
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Db 95 TCGGGCCACCAAGTGTGATGAGTACACATCTTTTCGACAGAGTGCCTTAAG 154
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QY 171 aaaaacacagacaaactttaaaatgtgcaatgtttcacagcaggaagcagatgga 230
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Db 155 AAAACACAGACAACTTTAAATAATGGCAATGTTTACACAGCAGAGACGAGGGA 214
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QY 231 ttgacctatgacctatgaagaataatgaacatttggcccggaagttaacagggcaca 290
|||||
Db 215 TTGCTTTATGACCTATTAGAAATATATACCATTTTGGCTCGAAGTTCAAGGCACA 274
|||||
QY 291 gactatccacatgttgaagaatcttctaagaatcatgtaattgaagaatatacgaaggag 350
|||||
Db 275 GACTATCCACATGTTGAGAAATTTTAAAGATCATGTAATGAGATATCAAGGAG 334
|||||
QY 351 gtggggatcgaagaatgtgatgataacacacagccttcaagatttcctgaactggc 410
|||||
Db 335 GTGGGATCGAAATATGTTATGATTAACAACAGCTCTTGAATTTCTCAACTTGCC 394
|||||
QY 411 acttaaaccttaccaggaaggttccagaattgagaaacacacataagaagacttcc 470
|||||
Db 395 ACTTAAACCTTACACGAGGATTCAGATTTGAGAAAAACACATATAGAACTTTTC 454
|||||
QY 471 caaagataaagatgacattttaattacgaacattctcgtagaactcctaagaagca 530
|||||
Db 455 CAAGATTAAGATGATGATTTTAAATATACGAACCTTTTCGTAGAACCTCTTAAAGCA 514
|||||
QY 531 tggattacattatctcagaagaatggtcgaggaataaagaacatga 575
|||||
Db 515 TGGATTACATTATCTCANGAAAAATGGCAGAAAAATTAACATGA 559
|||||

RESULT 2
LOCUS AQ280053/c 639 bp DNA GSS 22-NOV-1998
DEFINITION CITBI-EI-2511n5.TR CITBI-EI Homo sapiens genomic clone 2511n5,
genomic survey sequence.
ACCESSION AQ280053
VERSION AQ280053.1 GI:3905872
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 639)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,

Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H., Simon, M. and
 Venter, J. C.
 Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 Unpublished (1998)
 Other GSSs: CIBB1-E1-2511N5.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/hungen/Bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends

FEATURES

1. 639
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2511N5"
 /clone_lib="CIBB1-E1"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 186 a 102 c 107 g 244 t
 ORIGIN

Query Match 20.5%; Score 504.2; DB 100; Length 639;
 Best Local Similarity 95.7%; Pred. No. 7.1e-85;
 Matches 518; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

448 aaaaacacataagaagaactttcccaagaataagatgacattttaaattcgaactta 507
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 639 AAAAACACATAGAGAACTTTCCAAAGATAGATATTTTAAATGATGAAACTTA 580
 |||||||
 508 tctgtagaactcctaaaggcatggattacattatctcgaagaatggcagaataa 567
 |||||||
 579 TCTATGAAACTCTTAAGAACATGATTTACATTTATTCGGAATAATCCGAGAAATA 520
 |||||||
 568 aagcatgaataatcaatgaagatcaagaataatgcaattgataatagaactaagccag 627
 |||||||
 519 AAGCATGAATATCATATGAGATCAGAAATGCAATGATTAATAGAAACTTAAGCCAG 460
 |||||||
 628 gaagatgtgaagaagttggagatagttattctgactcactgcgaacatttaagt 687
 |||||||
 459 GAAGATGTTGAAGAAATTTGGAGATATGTTCTGATCTACCTGCACAAACATTTTAGT 400
 |||||||
 688 gtgcattccccaagaagaatgataatcccaaaagaatattcccaataataatgac 747
 |||||||
 399 GTGCCATCCTTAGAAGAGATCATTAATCCAAACAGATATTTCCCAATATATATGTAC 340
 |||||||
 748 aacatgccaataacaaagtcgtgagtagttactacaaacaaacagatgacctc 807
 |||||||
 339 AACATGGCCAAATACAGTAACATGGAGTACTTACACACAAACAAATCAGATGACCTC 280
 |||||||
 808 cctcaatggatattatctgcatagaagtgcctgaacaaatggccaagaagaatgatg 867
 |||||||
 279 CCTCACTGGGTATATCTGCATGAAAGTCTAGCAAAATTTGGCCAAAGATGATACG 220
 |||||||
 868 aataatcaacttattgtgattggaagagatgattcagaagaacatgcgaattattt 927
 |||||||
 219 AATATCCAACTATGTTGAGATTGAAACAGATATATTCACGACATACAGATTATTTT 160
 |||||||
 928 ctgaatcctcctgaacctctactacttcttaataataacgaattattgttaaacatttg 987
 |||||||
 159 CTAGATCTCTTGAACCTCTCCTTACTTTTGAATTTATGAAATTTTGTGACACTTTTG 100
 |||||||
 988 g 988

Db 99 G 99

RESULT 3
 AA807217
 LOCUS
 DEFINITION
 mRNA sequence.
 ACCESSION
 AA807217
 VERSION
 AA807217.1 GI:2876793
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 517)
 REFERENCE
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jan 19, 1998 this sequence version replaced gi:2150641.
 CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrr/image/image.html

FEATURES

1. 517
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:135174"
 /clone_lib="NCI-CGAP-CCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT7AD-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-RTTACCAATCTGAAGTGGAGCGGCGCTATTTTCTTTTCTTTT-
 3']. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 177 a 102 c 113 g 125 t
 ORIGIN

Query Match 20.3%; Score 501.2; DB 38; Length 517;
 Best Local Similarity 98.4%; Pred. No. 2.7e-84;
 Matches 506; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

51 aggaacgacacacgggagcctgacagacatgagagagcaggggtgctccgggacctta 110
 |||||||
 4 ATGGAGCGCACCGGGGCTCGACAGACCTATGAGAGAGTGGGTGCTCCGGGCGCTTA 63
 |||||||
 111 tcgggacacacgaagctgtggaatgattaccacatcttttcgagaggaatgctcctaag 170
 |||||||

Db 64 TCGGGCCACCAAGCTGTGAATCACTTACCATCTTTTCAGCAGCAAGATGCTTAA 123

Qy 171 aaaaacagacaacacatttaaaaaaatalagcaattgttcacagcaggaagcagtgga 230

Db 124 AGAACACAGACAAACACTTAAAAAATATGCAATTGTTCACAGCAGGAGAACAGCACTGGA 183

Qy 231 ttggcgtttgacctttagaataatagcaatttggccctggaagtaccagaagaaca 290

Db 184 ttggcgtttgacctttagaataatagcaatttggccctggaagtaccagaagaaca 243

Qy 291 gactatcacacgtttgaagaaatttcttaagaatcgttaattgaagataatcaaaagag 350

Db 244 GACTATCCAAAGCTTGAGGAATTTCTTAAGATCATGTATGAAGATATCAAAAGGAG 303

Qy 351 gtggggatcagaanaatcgttgatgataacaacaacagccttcagattcctgcacactgcgc 410

Db 304 GTGGGATCAGAAATGTGATGATTAACCAACGAGCTCTTCAGATTCTTCGCAACTTCGCC 363

Qy 411 actttaaacttaccacaggaagatccagaatttggaaaaaacaataagagaactttc 470

Db 464 ACTTAAACTCTTACCGAGAGGATTCAGCAATTGAGAAAGCAACATAGAGACTTTTC 423

Qy 471 caaagaataagataagcatttttaaatgaactatctcgtagaacctcctaaagagca 530

Db 424 CAAAGATAGAGTATGATTTTATAGATTAGCAAACTTATCTCGAGAACTCTTAAAGGCA 483

Qy 531 tggattacattatctcaggaanaatggcgagaaa 564

Db 484 TGGATTACATTATCTCAGGAAATGCGAGAAA 517

RESULT 4

LOCUS A1810084 503 bp mRNA EST 07-JUL-1999

DEFINITION w65c09.x1 Soares_NFL-T_GBC_S1 Homo sapiens cDNA clone

ACCESSION IMAGE:2360464 3', mRNA sequence.

VERSION A1810084

KEYWORDS A1810084.1 GI:5396650

SOURCE EST.

ORGANISM human.

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

TITLE Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 503)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Feb 17, 1998 this sequence version replaced gi:2889728.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: 400p from Gibco

High quality sequence stop: 457.

Location/Qualifiers

1..503

Location="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2360464"

/clone_lib="Soares_NFL-T_GBC_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with

a modified polylinker; Site: 1: Not I; Site: 2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NBHL19W, testis NHT, and B-cell

NCI-CGAP-GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

Query Match 20.3%; Score 499.8; DB 61; Length 503;

Best Local Similarity 99.6%; Pred. NO. 4.9e-84;

Matches 501; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1001 cccattagaggggttcacatgcgtctcaaatatgtgtgttactcccccac 1060

Db 503 CTCATTAGAGAGGGTTGCCATGCATGCTCTACACTTATGTTGTTTACTTCCCCAC 444

Qy 1061 caaatcgtagaagcttcaacttttaatgctgatgtattcccgaaatgagcaaatgttg 1120

Db 443 CAAATCGTAGAAGCTTCAACTTTAATGCGATGATTTCCGAAATGATCAAAATGTG 384

Qy 1121 atatgccaaacttataatgataatgagaggtcactatgataatcctttctc 1180

Db 383 ATATGCCAAACTTATATGATGCAATGAGGTACGAGGTCACTGATATACATCTTTCTC 324

Qy 1181 gatgtgttatgctgtcgaagaagtggatcttgatgagcttctgctggaagattg 1240

Db 323 GATGTGTATGCTGTCTGCTGTAAGAAGTGATCTTGATGATGACTTCTTCTGGAAGATTG 264

Qy 1241 ttcttctttaatgataatcaggaatcttcaaatccttacttaccagactg 1300

Db 263 TTTCTTTCTTATGATGATCATCATCAGAAATCTTCAGAGTACCTTACTACAGACTG 204

Qy 1301 cagctggaanaaaccttgaacttaacttaaaaaagagacatatgaaatccttgagatggac 1360

Db 203 CAGTGGAAAAACATCTTACTACTTAAAAAAAGGCAATATTGAAATCCTGAGATGGAC 144

Qy 1361 tattgccccttggcaacttaccatctgaagcagattagtcgaagagattgagtg 1420

Db 143 TATTGCTCCTTGGCACTTACTATCTGTAAGCAATATTAGTCTAGAGAGTTTGATG 84

Qy 1421 agcaaaaagtcttcaactcctcgaagctgcaattgcagaacttttagaataattatataa 1480

Db 83 AGCAAAAAGTTTCTACTCTCAAGCTCAATGCGAATTCAGACATATTATTATATAA 24

Qy 1481 acagagatttacccttaagag 1503

Db 23 ACAGGAGTTTACTCTCTAAAGAG 1

RESULT 5

LOCUS AA545060 692 bp mRNA EST 04-AUG-1997

DEFINITION vj91a10.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

ACCESSION IMAGE:944442 5', mRNA sequence.

VERSION AA545060

KEYWORDS AA545060.1 GI:2306134

SOURCE EST.

ORGANISM house mouse.

REFERENCE Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 692)

Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The Washu-HHMI Mouse EST Project

Unpublished (1996)

On May 5, 1995 this sequence version replaced gi:797839.

Contact: Marra M/Mouse EST Project

Washu-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Db	92	AGCACTTTGATAG--AAAGTTTCTACTCTTCATCGCTGCAATTCGAGCAACTTTAGAA	35
Oy	1468	aatattataaacaagagtttaccctctaaagg	1501
Db	34	AATATTATTAAACAGAGTTTACTCTCAAGG	1
RESULT	7		
AA756999/c			
LOCUS	ah4db09.s1	Soares_testis_NHT	29-DEC-1998
DEFINITION	ah4db09.s1	Soares_testis_NHT	Hom sapiens cDNA clone 1309433 3'
ACCESSION	AA756999		
VERSION	AA756999.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Hom sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 328)			
NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.		
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
Unpublished (1997)			
On Jan 19, 1998 this sequence version replaced gi:2151285.			
Contact: Robert Strausberg, Ph.D.			
Tel: (301) 496-1550			
Email: Robert.Strausberg@nih.gov			
CDNA Library Preparation by: M. Bento Soares, Ph.D., M. Fatima			
Bonaldo, Ph.D.			
CDNA Library Arrayed by: Greg Lennon, Ph.D.			
DNA Sequencing by: Washington University Genome Sequencing Center			
Clone distribution: NCI-CCAP clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
www.bio.llnl.gov/bbrp/image/image.html			
Insert Length: 570	Std Error: 0.00		
Seq primer: -40m13 fwd	ER from Amersham		
High quality sequence stop: 325.			
Location/Qualifiers			
1..328			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="1309433"			
/clone_lib="Soares_testis_NHT"			
/sex="male"			
/lab_host="DH10B"			
/note="vector: pTR73D-Pac (Pharmacia) with a modified			
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA			
was prepared from mRNA obtained from Clontech			
Laboratories, Inc., and primed with a Not I - oligo(dT)			
primer (5'			
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3')			
Double stranded cDNA was ligated to Eco RI adaptors			
(Pharmacia), digested with Not I and cloned into the Not I			
and Eco RI sites of the modified pTR73 vector. Library			
went through one round of normalization to Cots, and was			
constructed by Bento Soares and M. Fatima Bonaldo. "			
BASE COUNT	83 a	55 c	49 g 141 t
ORIGIN			
Query Match	13.2%	Score 326;	DB 38; Length 328;
Best Local Similarity	100.0%	Pred. No. 1.6e-51;	
Matches 326; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	1477	aaaaacagagtttcctcttaagaggaataaaaaaactaaacagtttcaagga	1536
Db	328	AAAAACAGGAGTTTACCTTTAAAGGAGAAACAAAAAATAAAACGTTTGAAGGA	269
Oy	1537	tatctttgatatcagaanaagatttccaacacaggaagtgaaacagcacttttgt	1596
Db	268	TATCTTTGATATATCAGAAAGATTTTCACACGAGACAGTGAAGCAACCACTTTTGGT	209

QY	1597	gacaaacctcaatcaatgcaaccacaaatgctgtgttttaagaacaaccagaagttccgtgctta	1596
Db	208	GACAAACCTACATCATACCAACCAATGCTGTGATTTTAAAGAAACCAAAAGTTCCGTAGTCTA	149
QY	1657	agataacactggaattaaaaattgttgaaactgtgtggaactgttggaactttgataatgaagccat	1716
Db	148	ACATACCTACTGCAATTTAAATTTATGTAAATACCTTGTGGAAGCTTTGATTAATGAAGCCAT	89
QY	1717	atctgagaatgtagctactcaaaaagaagctgtcattcaataaagcattcttaataaac	1776
Db	88	ATCTAGAGATGAGCTACTACTCAAAAGGAGTCTGTCATTAATGAAGTATTTCTAATAATAAC	29
QY	1777	acattatgaagaagtcgcaaatat	1802
Db	28	ACATTATGTAAAGGAGTCCAAAATA	3
RESULT	8		
LOCUS	AA825936	482 bp	mRNA
DEFINITION	cd39h06.s1	NCI_CGAP_GCB1	Homo sapiens CDNA clone IMAGE:137283 3'
ACCESSION	AA825936		
VERSION	AA825936.1	GI:2899248	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 482)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997)		
	On May 5, 1995 this sequence version replaced gi:797816.		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdnp/image/image.html		
	Insert Length: 701 Std Error: 0.00		
	Seq Primer: -40m13 fwd. ET from Amersham		
	High quality sequence stop: 479.		
FEATURES	Location/Qualifiers		
source	1..482		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:137283"		
	/clone_id="NCI_CGAP_GCB1"		
	/tissue_type="germinal center B cell"		
	/lab_host="DH10B"		
	/note="Vector: pUT3D-Pac (Pharmacia) with a modified polynker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for		

germinal center B cells by flow sorting (CD20⁺, IgD⁺), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - Oligo(dT) primer
 15'-TGTACCAATCTGAGTGGAGGCGGCTCTTTTCTTTTCTTTT-3'. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 144 a 73 c 97 g 168 t
 ORIGIN

Query Match 13.2%; Score 325; DB 39; Length 482;
 Best Local Similarity 100.0%; Pred. No. 2.3e-51;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

664 attcactctgaaccatttagtggtgctccatccctagaagaagtcataatcaaacaa 723
 482 ATCTACCTGCAACCATTTTGTGCTGCTCCATCCCTAGAAAGTCATTAATCAAAACAA 423
 724 gtaattcccatatataatgtaacatggaacataaagtaacggtgagtgatata 783
 422 GTAATTCCTCATATATATATGACATGCGCAATACAAAGTAACGTAAGTATATA 363
 784 ctacaaacaacatagatgacctccctcactcgtggtatattctgcataaagtcctaca 843
 362 CTACAAACAATATGATGACATGCTCCCTCAGTGGTATATATGCGATTAAGTCCCTACA 303
 844 aattggccaagaagaatgatatgaataaccactatgttgattgaaagagatgta 903
 302 AATTGGCCCAAGCAAGATATGATATATCACTTATGTGATTTGAACGAGATGTA 243
 904 ttcaagaacatcgaagatatttctctgaatctcctgaactctactacttgaatat 963
 242 TTCAGAAATGCGAGATTTATTTCTAGATCTCCCTGAACCTTACTTCTTGAATAT 183
 964 taagaattattgtaaacatttgg 988
 182 TACGATTTATTTGTAACATTTTG 158

RESULT 9
 A0376588 698 bp DNA GSS 29-JUN-1999
 LOCUS RPCI-11-161F2.T3 RPCI-11 Homo sapiens genomic clone RPCI-11-161F2,
 DEFINITION genomic survey sequence.
 VERSION A0376588
 KEYWORDS A0376588.1 GI:4347611
 SOURCE GSS.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 698)
 Zhaio, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and
 Venturi, J. C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-161F2.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org

library availability, please contact Pieter de Jong
 (pieter@jng.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1. 698
 /organism="Homo sapiens"
 /db_xref="GDB:7561561"
 /db_xref="taxon:9606"
 /clone="RPCI-11-161F2"
 /clone_1b="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 214 a 129 c 146 g 209 t
 ORIGIN

Query Match 12.7%; Score 312.4; DB 102; Length 698;
 Best Local Similarity 96.7%; Pred. No. 5.1e-49;
 Matches 319; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

989 gcttgctgcaaccctcatttagagaaggttgcacatgctctcagttatgttctgt 1048
 369 GTTGTGCGCAACCATTTAGAGGGTGGCATGATGCTGCTCACTTATGTGTTGT 428
 1049 tacttcccccacaaatcgtagaaggttcacttcaattgaatgcatatcccgaaatga 1108
 429 TATTTCCCTCCCAATCATAGAAAGCTTCACTTTTATGCGTATGTTTCCGAAATGA 488
 1109 gtcaaatgttgatatacccaactcactatgcatgcaatggtgacaggttcactgatac 1168
 489 GTCAAAATGTGATGATGCGCAAACTTCATGATGCAATGGGTGCGAGATCACTGTGATAC 548
 1169 atacccttctcgatggtgtgtatgctgctgctgaagaagtgatctgtagagctcttg 1228
 549 ATACCGTTTCCAATGCTGTATGCTGCTGCTGAAGAAAGTGACCTTGATGACCTTCTTG 608
 1229 ctggaagatagttcttcttcttaatgatacgcacgaagaattctcaagctacctt 1288
 609 CTGGAGATTTAGTTCTTTCTTAATGATCATGATGAGGAATCTTCATGATCCCTCTT 668
 1289 actacagactcagtggaanaacactctg 1318
 669 ACTTGACAGCTGCAAGTGGAAACATCTTG 698

RESULT 10
 AA420348 387 bp mRNA EST 16-OCT-1997
 LOCUS AA420348
 DEFINITION VD01402.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
 IMAGE:791282 5', mRNA sequence.
 ACCESSION AA420348
 VERSION AA420348.1 GI:2080825
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Scuriognath; Muridae; Murinae; Mus.
 1 (bases 1 to 387)
 Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Gettel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 On Sep 12, 1996 this sequence version replaced gi:1394414.
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1394414.
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:475690
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers

FEATURES

source

1. 387

/organism="Mus musculus"

/strain="B6D2 F1/J"

/db_xref="taxon:10090"

/clone="IMAGE:791282"

/clone_lib="Knowles Solter mouse 2 cell"

/tissue_type="embryo"

/dev_stage="2-cell"

/lab_host="DH10B"

/note="Organ: embryo; Vector: pluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(5'): 5'-CGGTGCGCCGTCGACGCTTTTCTTTT-3'.
CDNAs
were cloned into the MluI/SalI sites of a modified
pluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

BASE COUNT 122 a 79 c 79 g 107 t
ORIGIN

Query Match 11.0%; Score 271; DB 33; Length 387;
Best Local Similarity 88.1%; Pred. No. 3e-41;
Matches 295; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 79 atggaagtcgaaggtgtgctcccgagccctacgagccacgaagctgtgaatgaatt 138
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 53 ATGAGCGCTAGGCGTCTCTCTTGACCTTACCGGCCACAGCTGTGATGAGTA 112
QY 139 accacatcttctcgagcaagaatgctcttaagaacaacagacacatttaaaatat 198
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 ACCACATCTTTTGGATGAGATGCCCTTAAAGAAACATGACACATTTAAATAAT 172
QY 199 ggaatgtgttcacagaggaagcagtgatgtgcttatactataaataaat 258
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 AGCAATTTGTTCACTGCAAGTTGAAGCTATGATGCTTATATCTTAAAGAGTAAT 232
QY 259 agcaatttgctcctgaagtlacaagcaacacactataccaactgttgaagaattctt 318
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 233 AGTAATTTTGCTCTGCTGAGTTACAGACACACACTATTCACTATTGAAAAATTTCTT 292
QY 319 aagaatcatgttaattgaagatcaaaaggagggtgggagatcagaataaagtgtgataac 378
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 293 AAGAATCATGTGATGATGAGATCAAGATCAAGGATGAGGATCGAAGCCCTTGATGACAAAC 352
QY 379 aaccagctcttcagattctcgtgaacttcgcact 413
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 353 AATCAACTATTCAGATTTCTGCAACTTCTCCACT 387

RESULT 11

AA907054

LOCUS AA907054 361 bp mRNA EST 10-JUN-1998

DEFINITION omig08.s1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone

IMAGE:1540670 3', mRNA sequence.

ACCESSION AA907054

VERSION AA907054.1 GI:3042514

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 361)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
Unpublished (1997)
COMMENT On Jan 14, 1998 this sequence version replaced gi:1797337.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 128 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 350.
Location/Qualifiers

FEATURES

source

1. 361

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1540670"

/clone_lib="Soares_NFL_T_GBC_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 128 a 71 c 78 g 84 t
ORIGIN

Query Match 10.9%; Score 269.4; DB 39; Length 361;
Best Local Similarity 99.6%; Pred. No. 6e-41;
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 390 cgaattccctgcaacttcgcccacttaaacctacacaggaagatccgaattagaa 449
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 CTGATTTCTCGCACTGCGCCACTTAAACTCTACACAGAGTATCCGATTTAGAAA 150
QY 450 aaacaacatagagaacttcccaagataaagatgcatctttaaactaagaactatc 509
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 AAACAACATGAGAACTTTCCAAAGATTAAGATGCAATTTTAATTAACGAACCTTATC 210
QY 510 tcgtgaactcctaaaggcatggaattacattatctcaggaataatggcgagaataa 569
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 211 TCGTGAACCTCTTAAAGCATGAGATTACATTATCTCAGAAAATGGCGAATAATANA 270
QY 570 gcatgaataatcaatgaagatcaagaanaatgcaattgataaagaactaagccaga 629
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 271 GCATGAATTAATCAATGAAGATCAAGAAATGCATTTGATATAGAACTAAGCAGAGA 330
QY 630 agatgttgaagaagattggagatatgtatt 660
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 331 AGATGTTGAAGAAGTTTGGAGATATGTTATT 361

RESULT 12

AQ261251/c

LOCUS AQ261251 378 bp DNA GSS 24-OCT-1998

DEFINITION CITBI-EI-2506G1.TR CITBI-EI Homo sapiens genomic clone 2506G1,

genomic survey sequence.

ACCESSION AQ261251

VERSION AQ261251.1 GI:3787775

KEYWORDS GSS

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 378)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,

Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J. C.
 Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
 Map Building
 Unpublished (1998)
 Other-GSSs: CITR1-EL-2506G1.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mda@amg.tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/hungen/Bac_end_search/Bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..378
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2506G1"
 /clone_lib="CITR1-EL"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
 BASE COUNT 119 a 61 c 71 g 127 t
 ORIGIN

Query Match 10.5%; Score 258.2; DB 100; Length 378;
 Best Local Similarity 93.7%; Pred. No. 7.4e-39;
 Matches 269; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 702 agaaagtcataatccaaacaaagtaattcccaatataatgatacaacatggcccaatc 761
 |||
 DB 377 AGAAGTCATTAATCAAACTACTAATTCCTCTATATATATGACAACTGCGCAATAC 318
 QY 762 aaataaagcggagtgatgatacaaaaacaaatagagactccctcactgggatt 821
 |||
 DB 317 AACTTAACATGAGAGTACTACACAAATCAATCAATGAGACCTCCCTACGGGATT 258
 QY 822 atctgcataaagtcctagcaaatgcccagaagcaatgataatgataatccaaacta 881
 |||
 DB 257 ATGTGCATGAATGCTCTAGCAATATGGCCAAAGTGAATGATACGATATCCGACTTA 198
 QY 882 tgltgattgaagcagatgatlacagaaacatcgcaattatcttctagatctccctga 941
 |||
 DB 197 TGTGTGATTGAACAAGATATATTCAGACAAATCAGAGATTATTTCTAGATCTCTGA 138
 QY 942 acctctactactttgataatgaatgaattattgttaaacatttgg 988
 |||
 DB 137 ACCTCTCTTACTTTGAATATATGAAATATTGTCGACATTTTG 91

RESULT 13

LOCUS AO791096 496 bp DNA GSS 03-AUG-1999
 DEFINITION HS_2189_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=9 Row=L, genomic survey sequence.
 ACCESSION AO791096
 VERSION AO791096.1 GI:5698720
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 496)
 AUTHORS Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, D., Young, D., Zhao, S., Adams, M. D. and

Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589
 On Sep 10, 1998 this sequence version replaced gi:3552083.
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 2189 row: L column: 9
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 496.

FEATURES

Location/Qualifiers
 1..496
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=2189 Col=9 Row=L"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 159 a 91 c 91 g 150 t 5 others
 ORIGIN

Query Match 8.4%; Score 206.2; DB 87; Length 496;
 Best Local Similarity 91.2%; Pred. No. 3.8e-29;
 Matches 229; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

QY 1122 tatgccaaacttcacatgatgcaatggtacgagtgatcactgatgataacactttctcg 1181
 |||
 DB 83 TATGTCAAACTTCATGATGATGCAATGGCATGATATCACCAGATGATACCTTTCTCG 142
 QY 1182 agtggatgatactgctgacgaagaagtgtactcttgatgagctcttcctcggaagattgt 1241
 |||
 DB 143 ATGTGTCTATCTCTGCTGCAAAAAGTGGATCTGTGTAAGCTTCTTGGGAAGATTACT 202
 QY 1242 tctcttctaagtgatcatcatcagcaaatcttcaagaccctctactacagacgc 1301
 |||
 DB 203 NCTTCTTACGATGATCATCATCAGAAATTTCTCAAGTACCACTTATTACAGACTGC 262
 QY 1302 agtggaaaaacatcttgactacttaaaaaagggacatatgtgaaaatcctggaatggact 1361
 |||
 DB 263 AGTGGAAAAACATCTGTGATACTTAAAAAAGGACATATTGAAAATC--TGAGATGAGACT 320
 QY 1362 atttgctcctt 1372
 |||
 DB 321 ATMTGTTCTTT 331

RESULT 14

LOCUS AA240712 501 bp mRNA EST 12-MAR-1997
 DEFINITION mv30b11.r1 Guaywoodford Beiler mouse kidney day 0 Mus musculus CDNA clone IMAGE:656541 5', mRNA sequence.
 ACCESSION AA240712
 VERSION AA240712.1 GI:1865087
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 501)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

TITLE Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 JOURNAL The Washu-HMI Mouse EST Project
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1402298.
 Contact: Marra M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:402389
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 437.

FEATURES

SOURCE

1. 501
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:656541"
 /tissue_type="kidney"
 /dev_stage="newborn (day 0)"
 /lab_host="SOLR (Kanamycin resistant)"
 /note="Organ: kidney; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
 -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Library provided
 Lisa Guay-Woodford."

BASE COUNT 125 a 115 c 125 g 136 t
 ORIGIN

Query Match 7.5%; Score 185; DB 30; Length 501;
 Best Local Similarity 62.0%; Pred. No. 3.5e-25;
 Matches 313; Conservative 0; Mismatches 185; Indels 7; Gaps 1;

Oy 779 ttatctcaaaacaaacagatgagctccctccactggtatctatctccatgaagtc 838
 Db 1 TCATCTTGACGACACAGTCGAAAGACTTCTCACTGGCTCTGACCTGAAAGT 60
 Oy 839 tagcaaatgagcaagcaatgatgatgaataacacactatgttgattgaagag 898
 Db 61 TGGCAAAATTGGCCCAAGCTGACAGACTGGAAGCAGCAGTATGACTGGATTGGAAG 120
 Oy 899 atgtatcagaacaacgcagatatttcttagatctccctgaaccttacttcttg 958
 Db 121 ATGCTTTAGACTATACAGATTTACTATGTGTCACCTAAGAGCAGCAGTCTCAAT 180
 Oy 959 aatattacgaattattttaacatttggagctgtcgaacctatttagagaggttg 1018
 Db 181 ATCTTTTGAAGCTTTCCTCAAGCTTGAAGTTTCTGC-----CGAAGGAAACGG 233
 Oy 1019 ccatgatgctctacagatgatgttctgttacttcccccacacacatgataagcttc 1078
 Db 224 CCATGAGAGCAATTCAGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 293
 Oy 1079 aacttttaatgcgatgtatcccgaaatgagtcacaaatgttgatatagccaaactcatg 1138
 Db 294 AGCTTTTATGATGAGATGATGCGAGAGATCTGCTTAACAGAGAGATGCCCATCTGAG 353
 Oy 1139 atgcaatggatgagaggtgcacatgataacatacttcttcgatgtgtgtatgtctg 1198
 Db 354 ATGGCTTGCGACCCGACACATGATGATGATGATGATGATGATGATGATGATGAT 413
 Oy 1199 ctgaagaagtgtatctatgagctctctgctggaagatgattcttcttcaatgagtc 1258
 Db 414 AGGATGAAGTATGACTTAACTAGTTACTAGCTGCTGATGTGTGTCATTTCTGATGAG 473

Oy 1259 atcatcagaatctctcaagttacc 1283
 Db 474 ATTACAGAGACTTCTGAAAGTCC 498

RESULT 15

LOCUS AO415970 564 bp DNA GSS 23-MAR-1999
 DEFINITION RPCI-11-207H10.TJ RPCI-11 Homo sapiens genomic clone
 RPCI-11-207H10, genomic survey sequence.
 ACCESSION AO415970
 VERSION AO415970.1 GI:4474939
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 564)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
 Venter, J.C.
 Use of BAC End Sequences from library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-207H10.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@ig.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: SP6
 Class: BAC ends.

JOURNAL
 COMMENT
 TITLE
 REFERENCE
 AUTHORS

FEATURES

SOURCE

Location/Qualifiers

1. 564

/organism="Homo sapiens"
 /db_xref="GDB:7579281"
 /db_xref="taxon:9606"
 /clone="RPCI-11-207H10"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 179 a 106 c 116 g 161 t 2 others
 ORIGIN

Query Match 7.1%; Score 174.2; DB 102; Length 564;
 Best Local Similarity 92.4%; Pred. No. 3.6e-23;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 989 gcttcgcgaaccctattagagaggttgcacatgctctcacaattatgttgttg 1048
 Db 368 GTTGTGCGAACCCTATTGAGAGGGTTGCCATGATGGCTACATTTGTGCTTGT 427
 Oy 1049 tacttcccccaacacgtagaagcttcaactttaatgctatgattccgaaatga 1108
 Db 428 TACTTCCGCCAACCAATTGAGAAAGCTTCAACCTTTAAAGCGATATTTCCCAATGA 467
 Oy 1109 gtcaaatgttgatagcccaactcaatgatgaatgagaggtgacatgataac 1168
 Db 488 GTCAAAATGTTGATATGTCACAACTTCATGATGATGATGATGATGATGATG 547
 Oy 1169 ataccttctcgatgt 1185
 Db 548 ATACCTTTCTCGATGT 564

. Fri Mar 24 13:38:35 2000

us-09-183-789-43.rst

Page 11

Search completed: March 23, 2000, 21:52:11
Job time: 8155 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 13:19:52 ; Search time 172.6 Seconds
(without alignments)
1385.209 Million cell updates/sec

Title: US-09-183-789-38_COPY_1_1997

Sequence: 1 ctactataggagagaccac.....tctctgttaagtaaaagctgc 1997

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 428588

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/5C_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/5D_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/5E_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/5F_COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/5G_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.6	3.5	6420	3	US-08-374-483-1
2	66.8	3.3	4525	3	US-08-613-861-2
3	59.6	3.0	1123	1	US-08-458-0238-3
4	59.4	3.0	7218	1	US-08-232-463-14
5	56.2	2.8	1700	4	US-08-839-581A-1
6	52.6	2.6	9592	1	US-08-393-734-3
7	52.2	2.6	120	3	US-08-454-557C-76
8	52.2	2.6	120	4	US-08-340-426D-76
9	52.2	2.6	120	4	US-08-430-673C-76
10	52.2	2.6	120	4	US-08-340-426D-76
11	52.2	2.6	3984	1	PCT-US95-17111A-76
12	51.4	2.6	9837	2	US-08-832-883-68
13	51.4	2.6	9837	2	US-08-832-877-68
14	50	2.5	4059	3	US-08-252-493C-4
15	50	2.5	4059	3	PCT-US95-07534-4
16	50	2.5	4059	3	PCT-US95-05611A-11
17	48.8	2.4	4982	4	US-08-900-148-1
18	48.2	2.4	1672	1	US-08-594-031-154
19	47.2	2.4	1672	1	US-08-172-331B-13
20	46.8	2.3	115	3	US-08-454-557C-75
21	46.8	2.3	115	4	US-08-340-426D-75
22	46.8	2.3	115	4	US-08-450-673C-75
23	46.8	2.3	115	4	PCT-US95-17111A-75
24	42.6	2.1	8299	2	US-08-462-014-2
25	40.4	2.0	1425	1	US-07-715-184-3
26	40.4	2.0	1425	1	US-07-876-280-6
27	40.4	2.0	1425	1	US-07-876-280-6

28	40.4	2.0	1425	1	US-07-935-310A-1	Sequence 1, Appl
29	40.4	2.0	1425	1	US-07-828-788A-1	Sequence 1, Appl
30	40.4	2.0	1425	1	US-08-049-783-3	Sequence 3, Appl
31	40.4	2.0	1425	1	US-08-147-189-1	Sequence 1, Appl
32	40.4	2.0	1425	2	US-08-316-301A-7	Sequence 7, Appl
33	40.4	2.0	1425	2	US-08-904-278-1	Sequence 1, Appl
34	40.4	2.0	1425	6	PCT-US92-03624-7	Sequence 7, Appl
35	40.4	2.0	1425	6	PCT-US92-11337-1	Sequence 1, Appl
36	40.4	2.0	1425	6	PCT-US93-07409-1	Sequence 1, Appl
37	36.4	1.8	3093	1	US-08-252-966B-19	Sequence 19, Appl
38	36	1.8	741	2	US-08-616-368A-2	Sequence 2, Appl
39	34.8	1.7	1405	1	US-07-710-361-3	Sequence 3, Appl
40	34.8	1.7	2210	1	US-07-710-361-2	Sequence 2, Appl
41	34.6	1.7	5183	2	US-08-459-568-3	Sequence 2, Appl
42	34.6	1.7	5183	2	US-08-399-411-3	Sequence 3, Appl
43	34	1.7	201	4	US-08-930-274-25	Sequence 25, Appl
44	33.8	1.7	5181	2	US-08-257-073-10	Sequence 10, Appl
45	32.8	1.6	2121	4	US-08-897-340-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-374-483-1
Sequence 1, Application US/08374483
Patent No. 5880102
GENERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
TITLE OF INVENTION: MICHAEL A.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-83
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-374-483-1

Query Match 3.5%; Score 69.6; DB 3; Length 6420;
Best Local Similarity 77.8%; Pred. No. 1.1e-10;
Matches 84; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ctactataggagagaccacgtctgttaccgagctctggtacacacgttaagccgcgcag 60
DB 975 ctactataggagagaccacgtctgttaccgagctctggtacacacgttaagccgcgcag 1034

OY 61 tgtgctggaagtgctcaaccagtgatattatttgacagcaactg 108
|||||
Db 1035 TGTGCTGGAATTAAATTCTGCAGATTTCATCCACTGCGCGGCGCTCG 1082

RESULT 2

US-08-613-861-2

Sequence 2, Application US/08613861

Patent No. 5843770

GENERAL INFORMATION:

APPLICANT: Ill, Charles R. et al.

TITLE OF INVENTION: Antisense Constructs Directed Against Viral Post-Transcriptio

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/613.861

FILING DATE: 13-APR-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/111.111

FILING DATE: 12-DEC-1909

ATTORNEY/AGENT INFORMATION:

NAME: Attorney, Name Init

REGISTRATION NUMBER: 000000

REFERENCE/DOCKET NUMBER: oe

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4525 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-613-861-2

Query Match

Best Local Similarity 3.3%; Score 66.8; DB 3; Length 4525;

Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ctcaataaggaagaccagctgtgctgacagctgagatccactagtaagcgccgacg 60
|||||
Db 3070 CTCACATAAGGAGACCAAGCTTGCTACCGAGCTGGATCCACTAGTAACGGCCGACAG 3129

OY 61 tgtgctgga 70
|||||
Db 3130 TGTGCTGGA 3139

RESULT 3

US-08-458-023B-3

Sequence 3, Application US/08458023B

Patent No. 5667990

GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Yoder, Wendy

APPLICANT: Takagi, Shinobu

APPLICANT: Booninathan, Karuppan C.

TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458.023B

FILING DATE: 01-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lowrey Dr., Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4086.010-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1123 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Humicola insolens

INDIVIDUAL ISOLATE: DSM 6595

FEATURE:

NAME/KEY: CDS

LOCATION: 126..806

US-08-458-023B-3

Query Match

Best Local Similarity 3.0%; Score 59.6; DB 1; Length 1123;

Matches 65; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 ctcaataaggaagaccagctgtgctgacagctgagatccactagtaagcgccgacg 60
|||||
Db 8 CTCACATAAGGAGATTAAAGCTTGCTACCGAGCTGGATCCACTAGTAACGGCCGACAG 67

OY 61 tgtgctggaagtg 74
|||||
Db 68 TGTGCTCTAAAGCG 81

RESULT 4

US-08-232-463-14/c

Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

```
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZPPT-F15
US-08-232-463-14
```

```
Query Match 3.0%; Score 59.4; DB 1; Length 7218;
Best Local Similarity 5.3%; Pred. No. 1,2e-07;
Matches 21; Conservative 220; Mismatches 156; Indels 0; Gaps 0;
```

```
QY 1495 tgcctcgcagtgaccaccagttacagtaatgcttcggtggaacgtgccaataac 1554
      ||| ||||| | | | | | | | | | | | | | | | | | | | | | |
DB 1474 TATCTATGCAGTAGTAAAGAGATAGAAATTGTGACRRRRRRRRRRRRRRRR 1415
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1555 accacaaatattccctgcctgccaataaataatgatgataataaataataat 1614
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1414 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1355
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1615 gaaagagttcgaaggttggccaataatgaagaatttcaattgcttgaagagt 1674
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 11354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1675 acaagatcctatgaagtcagaacattgttgaattacatcagaagagcaag 1734
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1294 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1235
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1735 gtttaaaagttgcttaattcagcaactcgaagagcgcttaagaataagattcca 1794
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1234 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1175
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1795 ctgcctcagaagaatgaagcatcgagaaaagaataattgttgaagcaagacca 1854
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1855 aggaagaacaagacatatgcttgaagatgaaacag 1891
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1078
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 5
US-08-839-581A-1/C
Sequence 1, Application US/08839581A
Patent No. 5958705
GENERAL INFORMATION:
APPLICANT: Staunton, Donald E.
APPLICANT: Lipsky, Brian P.
```

```
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding/Signaling
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,581A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/33886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 283..1482
US-08-839-581A-1
```

```
Query Match 2.8%; Score 56.2; DB 4; Length 1700;
Best Local Similarity 83.1%; Pred. No. 4,7e-07;
Matches 64; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 ccacgcttgtagcagcgtcgcagttccactagtaacgcccagtgctggaagtggt 76
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1691 CCACGCTGTGACGAGCTCGATCCACTAGTAACGGGCGCAGTGTGCTTAAGTTAC 1632
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 77 caaccagtgattatta 93
      ||| ||| ||| |||
DB 1631 CAACAGCTGTTAATTA 1615
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 6
US-08-839-734-3
Sequence 3, Application US/08393734
Patent No. 5652224
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Kozarsky, Karen F.
APPLICANT: Strauss, Jerome F.
TITLE OF INVENTION: Methods and Compositions for Gene
TITLE OF INVENTION: Therapy for the Treatment of Defects in Lipoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,734
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: UPNH1254USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9592 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US 393-734-3

Query Match 2.6%; Score 52.6; DB 1; Length 9592;
Best Local Similarity 86.6%; Pred. No. 1.4e-05;
Matches 58; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 actaaggagaccacgctgtgtacccgagctcgatccactagtaacggccgcaagtgt 63
Db 4092 ACCTTGGCTGATCAACCTTGTCGCCAGCTCGATCCACTAGTAACGGCCGCAAGT 4151

QY 64 gctggaa 70
Db 4152 GCTGGAA 4158

RESULT 7

US-08-454-557C-76/C
Sequence 76, Application US/08454557C
Patent No. 5830670

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,557C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609, 3840003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 base pairs

TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-76

Query Match 2.6%; Score 52.2; DB 3; Length 120;
Best Local Similarity 71.1%; Pred. No. 1.7e-06;
Matches 69; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 actaaggagaccacgctgtgtacccgagctcgatccactagtaacggccgcaagtgt 63
Db 98 ACTCAAGCTATGATCAACCTTGTCGCCAGCTCGATCCACTAGTAACGGCTGCCAGTGT 39

QY 64 gctggaaagtgtcaaccagtgattatttgaca 100
Db 38 GCTGTAAGTATACAAATATATTGTATATGCTATATA 2

RESULT 8

US-08-340-426D-76/C
Sequence 76, Application US/08340426D
Patent No. 5948634

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609, 3840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

US-08-340-426D-76

Query Match 2.6%; Score 52.2; DB 4; Length 120;
Best Local Similarity 71.1%; Pred. No. 1.7e-06;
Matches 69; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 4 actaaggagaccacgctgtgtacccgagctcgatccactagtaacggccgcaagtgt 63
Db 98 ACTCAAGCTATGATCAACCTTGTCGCCAGCTCGATCCACTAGTAACGGCTGCCAGTGT 39

QY 64 gctggaaagtgtcaaccagtgattatttgaca 100
Db 38 GCTGTAAGTATACAAATATATTGTATATGCTATATA 2


```

MEDICAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609,3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEO ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
PCT-US95-17111A-76

Query Match 2.6%; Score 52.2; DB 6; Length 120;
Best Local Similarity 71.1%; Pred. No. 1.7e-06;
Matches 69; Conservative 0; Mismatches 28; Indels 0; Gaps 0.

QY 4 actatagggaacccacgcgtgtgacgcagctcgatccactcagtagaagggccgcagcagt 63
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 98 ACTCAAGGTATGACATCAACTGTGTACCGAGCTCGATCCACTAGTAAGCGCTCCAGTGT 39

QY 64 gctgaaagtgtcaaccacagtgatattatttgcaca 100
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 38 GCTCAAGGTATACATATATTGTTATTTGTCATA 2

RESULT 11

```

RESULT 11
 US-08-040-753-1
 Sequence 1, Application US/08040753
 Patent No. 5464745
 GENERAL INFORMATION:
 APPLICANT: Mierendorf, Robert
 APPLICANT: Garber, Richard
 APPLICANT: No. 5464745Y, Robert
 APPLICANT: Hammer, Beth
 TITLE OF INVENTION: Protein Ligand Binding
 TITLE OF INVENTION: Region Mapping System
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles and Brady
 STREET: 1 South Pinckney St., Box 2113
 CITY: Madison
 STATE: WI
 COUNTRY: USA
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/040,753
 FILING DATE: 19930331
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 70-399-9001-1
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3984 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pTOPE-1b(+)
FEATURE:
NAME/KEY: promoter
LOCATION: 67..85
OTHER INFORMATION: /function= "T7 Promoter"
FEATURE:
NAME/KEY: RBS
LOCATION: 134..139
OTHER INFORMATION: /product= "5' end of T7 gene 10"
OTHER INFORMATION: fusion protein"/note= "This coding region is interrupted during cloning by insertion of putative epitope encoding
OTHER INFORMATION: DNA. "
US-08-040-753-1

Query Match 2.6%; Score 52.2; DB 1; Length 3984;
Best Local Similarity 94.7%; Pred. No. 1.1e-05;
Matches 54; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 14 gaccacgcgttgagccagagctcgatccactgtaacgagccgagctgtgcctgga 70
|||
DB 931 GATTCAAGCTTGTCGACCGAGCTCGATCCACTAGTACGGCCGCGAGTGTGCGAA 987

RESULT 12
US-08-832-883-68
Sequence 68; Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
APPLICANT: Baldi, Alphonso
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549

```

: INFORMATION FOR SEQ ID NO: 68:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9837 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-832-883-68

Query Match
Best Local Similarity 98.1%; Score 51.4; DB 2: Length 9837;
Matches 52; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 18 cagccttgtagcagagctcgatccactagtaacgagccgacagtgctgtgaa 70
|||
Db 7170 CAAGCTGTGTACCGAGCTCGATCCACTAGTAACGAGCCCGCAGTGTCTGGA 7222

RESULT 13
US-08-832-877-68
: Sequence 68, Application US/08832877
: Patent No. 5840506
: GENERAL INFORMATION:
: APPLICANT: Giordano, Antonio
: TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
: TITLE OF INVENTION: CANCER
: NUMBER OF SEQUENCES: 116
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P. C.
: STREET: Suite 1800
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,877
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-877-68

Query Match
Best Local Similarity 98.1%; Score 51.4; DB 3: Length 9837;
Matches 52; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 cagccttgtagcagagctcgatccactagtaacgagccgacagtgctgtgaa 70
|||
Db 7170 CAAGCTGTGTACCGAGCTCGATCCACTAGTAACGAGCCCGCAGTGTCTGGA 7222

RESULT 14
US-08-252-493C-4
: Sequence 4, Application US/08252493C

```

Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Mattis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-1 Eukaryotic
Expression Vector
US-08-252-493C-4

Query Match 2.5%; Score 50; DB 3; Length 4059;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 gcttgtagcagagctcgatccactagtaacgagccgacagtgtctggaa 70
|||||
Db 1027 GCTTGtagcagagctcgatccactagtaacgagccgacagtgtctggaa 1076

RESULT 15
PCT-US95-07554-4
Sequence 4, Application PC/TUS9507554
GENERAL INFORMATION:
APPLICANT: Sandrin, Mauro S.
APPLICANT: Fodor, William L.
APPLICANT: Rother, Russell P.
APPLICANT: Squinto, Stephen P.
APPLICANT: McKenzie, Ian F. C.
TITLE OF INVENTION: Methods for Reducing
Hyperacute Rejection of Xenografts
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA

ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: Dell 486/50
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07554
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260,201
FILING DATE: June 15, 1994
CLASSIFICATION:
APPLICATION NUMBER: 08/278,282
FILING DATE: July 21, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-144.1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-1400
TELEFAX: (203) 254-1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4059 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Apex-1 Eukaryotic
ANTI-SENSE: No
PCT-US95-07554-4

Query Match 2.5%; Score 50; DB 6; Length 4059;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 gcttgtagcagagctcgatccactagtaacgagccgacagtgtctggaa 70
|||||
Db 1027 GCTTGtagcagagctcgatccactagtaacgagccgacagtgtctggaa 1076

Search completed: March 24, 2000, 13:20:42
Job time: 8033 sec

Fri Mar 24 13:38:24 2000

us-09-183-789-38_copy_1_1997.rni

RESULT 1
 US-08-374-483-1
 ; Sequence 1, Application US/08374483
 ; Patent No. 5880102
 ; GENERAL INFORMATION:
 ; APPLICANT: GEORGE, SAMUEL E.
 ; APPLICANT: BLAZING, MICHAEL A.
 ; TITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,483
 ; FILING DATE: 17-JAN-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILSON, MARY J.
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 1579-83
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4000
 ; TELEFAX: (703) 816-4100
 ; TELEX: 200797 NIXN UR
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6420 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-374-483-1

Query Match 3.5%; Score 69.6; DB 3; Length 6420;
 Best Local Similarity 77.8%; Pred. No. 1.1e-10;
 Matches 84; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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 Db 975 CTCACATAGGGAGACCCAAGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAG 1034

'89-38_

QY 61 tgtgctggaaagtgttcaaccagtgattattttttgacagcaactgg 108
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 Db 1035 TGTGCTGGAATTAATTCTGCAGATATCCATCACACTGGCGGCCGCTCG 1082

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ESULT 13

S-08-040-753-1

Sequence 1, Application US/08040753

Patent No. 5464745

GENERAL INFORMATION:

APPLICANT: Mierendorf, Robert

APPLICANT: Gardner, Richard

APPLICANT: No. 5464745, Robert

APPLICANT: Hammer, Beth

TITLE OF INVENTION: Protein Ligand Binding

TITLE OF INVENTION: Region Mapping System

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles and Brady

STREET: 1 South Pinckney St., Box 2113

CITY: Madison

STATE: WI

COUNTRY: USA

33701-2113

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ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: pTOPE-1b(+)

FEATURE:

NAME/KEY: Promoter

LOCATION: 67..85

OTHER INFORMATION:

FEATURE:

NAME/KEY: RBS

LOCATION: 134..139

FEATURE:

NAME/KEY: CDS

LOCATION: 148..1092

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RESULT 14

US-08-252-493C-4

Sequencer

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US-08-040-753-1

Query Match

Best Local Similarity

Matches 50; Conservative

2.0%; Score 50; DB 1; Length 3984;

100.0%; Pred. No. 0.021;

0; Mismatches 0; Indels 0; Gaps 0;

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 Db 938 GCTTGTACCGAGCTCGATCCACTAGTAACGCCGCCAGTGTCTGCA 987

OTHER INFORMATION: fusion protein"/note-"This coding region is interrupted during cloning by insertion of putative epitope encoding DNA."

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JOURNAL
 ONLINE
 REFERENCE
 THORS
 FILE
 JOURNAL
 IDENT

Biotechniques 20 (1), 102-104 (1996)
 96366236
 2 (bases 1 to 5726)
 Lou, Y. and Holtz, A.
 Direct Submission
 Submitted (14-FEB-1997) CLONTECH Laboratories, Inc., 1020 East
 Meadow Circle, Palo Alto, CA 94303-8230, USA
 This vector can be obtained from CLONTECH Laboratories, Inc., 1020
 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
 call (415) 424-8222 or (800) 662-2566, extension 1. International
 customers, please contact your local distributor. For technical
 information, call (415) 424-8222 or (800) 662-2566, extension 3.
 This sequence has been compiled from information in the sequence
 databases, published literature and other sources, together with
 partial sequences obtained by CLONTECH. If you suspect there is an
 error in this sequence, please contact CLONTECH's Technical Service
 Department at (415) 424-8222 or (800) 662-2566, extension 3, or
 E-mail TECH@CLONTECH.COM.

Query Match	3.4%	Score 69	DB 14	Length 5726
Best Local Similarity	93.5%	Pred. No. 3.8e-06		
Matches	72	Conservative	0	Matches 5; Indels 0; Gaps 0
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Db	871	ctcactataggagaccacgcctgtgtaccagagctgataccactatgaagcgccag	930	
Qy	61	tgtgtcgtgaaagtgttc	77	
Db	931	tgtgtcgtgaaagtgttc	947	

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/product="hygromycin B phosphotransferase"
/protein_id="AAB49979.1"
/db_xref="gi:1899167"
/translation="MDRSKGPELTAISVERKFLIEKFDSPSLMQLSEGESEKRAFSFDV
GGRGVLYRNSGADGFFKDRIVYRHFSAALPIPEVLIDIGSESLYTCISRAGVAT
LQDLDELTELPAVLQPAEAMDAIAAIDLQTSQSGFPGEPGQIGQTYTRDFICIAADP
HYHMQYIWDVDFISASVAQALDELMLAEDCPPEVRAHLVHADFGSNNVLTQDGRITAVY
DMSLEAFDSDCEVANIFFMRPMLACMEQQRFEERHRLPELAGSPRLRAYVLTGIGLQD
LYQSLVDNCFDQDAWAQGRCDALVRSAGATGTRQIARRSAAVTDCVEVLADSGNR
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4730..5591
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complement(4730..5590)

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7								

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GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 24, 2000, 04:02:39 : Search time 5911.47 Seconds

(without alignments)
-1038.072 Million cell updates/sec

Title: US-09-183-789-38

Sequence: 1 ctcacatagggagaccac.....aaaaaaaaaaaaaaaaaaaaa 2021

Scoring table: IDENTITY_NDC

Searched: 821193 seqs, -1518192014 residues

Database: GenBank.*

Word size: 0

Number of hits that pass the threshold : 1642386

1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_om.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl1.*
10: gb_pl2.*
11: gb_pl3.*
12: gb_ro.*
13: gb_sts.*
14: gb_sy.*
15: gb_un.*
16: gb_vl.*
17: em_fun.*
18: em_hum1.*
19: em_hum2.*
20: em_in.*
21: em_om.*
22: em_or.*
23: em_ov.*
24: em_pat.*
25: em_ph.*
26: em_pl.*
27: em_ro.*
28: em_sts.*
29: em_sy.*
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31: em_vl.*
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33: gb_hgt2.*
34: gb_in1.*
35: gb_in2.*
36: em_ba1.*
37: em_ba2.*
38: em_hum3.*
39: em_hum4.*
40: gb_pl4.*
41: gb_hgt3.*
42: gb_hgt4.*
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46: em_hgt1.*
47: em_hgt2.*
48: em_hgt3.*
49: em_hum5.*

50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	209.6	10.4	226280	41	AC011366	AC011366 Homo sapi
2	209.6	10.4	215387	42	AC008417	AC008417 Homo sapi
3	119.2	5.9	476	13	HS2282T	AL032554 H.sapiens
4	86.4	4.3	1738	10	HSB801162	AL117626 Homo sapi
5	86.4	4.3	3690	40	AF097645	AF097645 Homo sapi
6	84.8	4.2	2110	40	AF141326	AF141326 Homo sapi
7	80	4.0	6346	12	MM057368	U57368 Mus musculi
8	69	3.4	5726	14	CYB86672	U89672 Cloning vec
9	68.4	3.4	6802	5	A49700	A49700 Sequence 6
10	68.4	3.4	10443	5	A58521	A58521 Sequence 25
11	68.4	3.4	3840	14	EVE132038	AJ132038 Expressio
12	68.4	3.4	3986	14	PCDNA32EO	X90639 Cloning vec
13	68.4	3.4	7290	14	XXU43958	U43958 Cloning vec
14	66.8	3.3	4525	5	AR062871	AR062871 Sequence
15	62.2	3.1	7218	5	I66494	I66494 Sequence 14
16	60.4	3.0	161	10	HS031738	U31738 Homo sapien
17	59.6	2.9	1123	5	I65436	I65436 Sequence 3
18	55.8	2.9	184553	43	AC013452	AC013452 Homo sapi
19	55.2	2.8	510	13	G12382	G12382 UNH231 Tila
20	54.8	2.7	202342	41	AC009473	AC009473 Homo sapi
21	54.4	2.7	175133	42	AF018054	AF018054 Unculture
22	53.6	2.7	175133	42	AC010978	AC010978 Homo sapi
23	53.4	2.6	689	2	AF018044	AF018044 Unculture
24	53.2	2.6	175153	42	AC010978	AC010978 Homo sapi
25	53	2.6	1102	8	AF137070	AF137070 Sphenosty
26	53	2.6	173630	42	AC010902	AC010902 Homo sapi
27	52.6	2.6	9582	5	I58669	I58669 Sequence 3
28	52.6	2.6	357	13	G31347	G31347 UNH-009 T11
29	52.6	2.6	162575	33	AC004086	AC004086 Homo sapi
30	52.6	2.6	52359	41	AC010772	AC010772 Homo sapi
31	52.4	2.6	719	2	AF018052	AF018052 Unculture
32	52.4	2.6	731	2	AF018053	AF018053 Unculture
33	52.4	2.6	339	2	AF114621	AF114621 Unculture
34	52.4	2.6	1566	8	AF131673	AF131673 Zea mays
35	52.4	2.6	1623	8	AF131683	AF131683 Zea mays
36	52.4	2.6	3418	9	HSP58NRC	AJ000542 Homo sapi
37	52.4	2.6	1577	10	AB029348	AB029348 Homo sapi
38	52.4	2.6	4224	12	AF033115	AF033115 Mus muscu
39	52.4	2.6	1673	12	D88984S01	D88984 Mus musculi
40	52.4	2.6	3942	14	AF073995	AF073995 Vibrio ch
41	52.4	2.6	1199	16	DVG93295	U93295 Dengue viru
42	52.4	2.6	1197	16	DVG93301	U93301 Dengue viru
43	52.4	2.6	1200	16	DVG93302	U93302 Dengue viru
44	52.2	2.6	120	5	AR051506	AR051506 Sequence
45	52.2	2.6	3984	5	I15353	I15353 Sequence 1

ALIGNMENTS

RESULT 1
AC011366
LOCUS
DEFINITION Homo sapiens chromosome 5 clone Ctr-HSPC_568121, *** SEQUENCING IN
AC011366 226280 bp DNA HTG 06-OCT-1999
AC011366
VERSION AC011366.1 GI:6013575
KEYWORDS
HTG; HTG_PHAISEI.
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 226280)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 226280)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94596, USA
www.jgi.doe.gov.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 82 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 645: contig of 645 bp in length
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* 646 1347: contig of 702 bp in length
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* 2002 2675: contig of 674 bp in length
* 2002 2675: contig of 674 bp in length
* 2676 3336: contig of 661 bp in length
* 2676 3336: contig of 661 bp in length
* 3337 3966: contig of 630 bp in length
* 3337 3966: contig of 630 bp in length
* 3967 4625: contig of 659 bp in length
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* 4626 5279: contig of 654 bp in length
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* 5280 5967: contig of 688 bp in length
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* 5968 6664: contig of 697 bp in length
* 5968 6664: contig of 697 bp in length
* 6665 7351: contig of 687 bp in length
* 6665 7351: contig of 687 bp in length
* 7352 8034: contig of 683 bp in length
* 7352 8034: contig of 683 bp in length
* 8035 8717: contig of 683 bp in length
* 8035 8717: contig of 683 bp in length
* 8718 9374: contig of 657 bp in length
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* 9375 10049: contig of 675 bp in length
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* 10050 10721: contig of 672 bp in length
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* 10722 11432: contig of 711 bp in length
* 10722 11432: contig of 711 bp in length
* 11433 12070: contig of 638 bp in length
* 11433 12070: contig of 638 bp in length
* 12071 12682: contig of 612 bp in length
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* 12683 13282: contig of 600 bp in length
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* 14328 14983: contig of 656 bp in length
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* 19450 19624: contig of 175 bp in length
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* 36427 37156: contig of 730 bp in length
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* 37913 38580: contig of 668 bp in length
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* 41846 42243: contig of 398 bp in length
* 42244 42331: contig of 88 bp in length
* 42332 43453: contig of 1122 bp in length
* 43454 43550: contig of 97 bp in length
* 43551 43653: contig of 103 bp in length
* 43654 44770: contig of 1117 bp in length
* 44771 45352: contig of 582 bp in length
* 45353 45730: contig of 378 bp in length
* 45731 46467: contig of 737 bp in length
* 46468 46598: contig of 131 bp in length
* 46599 47487: contig of 889 bp in length
* 47488 47849: contig of 362 bp in length
* 47850 73972: contig of 26123 bp in length
* 73973 100123: contig of 26151 bp in length
* 100124 226280: contig of 126157 bp in length.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CIT-HSPC_568121"
BASE COUNT 66991 a 46147 c 45719 g 64623 t 100 others
ORIGIN
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Query Match 10.4%: Score 209.6; DB 41; Length 226280;
Best Local Similarity 63.2%: Pred. No. 7.7e-39;
Matches 373; Conservative 0; Mismatches 184; Indels 33; Gaps 2;

QY 1366 tatgacagagacattgtatgaccaccacattgattcttctcaccgacttcacaag 1425
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Db 207374 TATGCGAGGAGATGTATTCCACCAAGCCAAATGATTCGGTTGATGATTCAGTGG 207433

QY 1426 tctcacaagaatgagatgctgttaccacactgataagtaattgctggtgaagcccaa 1485
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Db 207434 TTCCACCAAGATGGCTGTATGCGAAGAACTGTGAGAAATGCACCTGAGAGAAATCAT 207493

QY 1486 aaactcagtgcttcgcaagtgaccacacagttacagtaattgcttcggtggaactgt 1545
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Db 207494 TACCACCAATTTCTCTGAGATGACCTAAAGTCACGAGAAAT----- 207536

QY 1546 gccacaatcacacaataatctcctgcacatgycgcaaaaaaataatgatataaata 1605
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Db 207536 -----ACTCCCTTTTCCAAATGTCAAGAAATGTAATGCTGATATAAATG 207583

QY 1606 tcaattaatgaagaagttgcaaggttgcgcaaaataatgaagaatttcatttgc 1665
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Db 207584 TCAATTATGTTAAGAGAAATTAACACTTATAGACGAAATATGAAAACTCTTCAATTCCT 207643

QY 1666 tgaagaggttcaagagatctatgaagtcagagacaaattgttgaattaccatcaaga 1725
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Db 207644 TGAAGGACTGCAAGGACCTATAGAACTCAAGAAATGATTTTGGATTCATCATCAAGGA 207703
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QY 1726 agcagcaaggtttaaaaaagtgtcttaattcaagcaactcgagaagcgcttaagaat 1785
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QY 1786 agattcccccctcacaagaagtaagcacatgagaaaaataattggttagtg 1845
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Db 207764 GATTTCGTGCTACTTGTTCAGAGAGATCATCTCACCGCAAAATGCATATCTGTTAATG 207823

QY 1846 ---caaaagcacaagaagaacacatagctgtagatgtagaaggttaattgctgaa 1902
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Db 207824 ACTGAGAGAGAAAAAAGATCAATATGCTGTTTCTAGAAATGAGAGAGATATGCTGAA 207883

QY 1903 gctccctataatctcgaatgaagaattcccttcacagaactagcaaa 1952
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Db 207884 GCCTCTACAGATGTTAGTGAATAAATGCGCTTCAGAGGCTAGACA 207933
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RESULT 2

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AC008417 215387 bp DNA HTG 31-OCT-1999
LOCUS Homo sapiens chromosome 5 clone CIT-HSPC_28708, *** SEQUENCING IN
DEFINITION PROGRESS ***, 5 ordered pieces.
ACCESSION AC008417
VERSION AC008417.2 GI:6165190
KEYWORDS HTG; HTGS_PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidi; Homo.
1 (bases 1 to 215387)
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REFERENCE DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
2 (bases 1 to 215387)
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
COMMENT Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Oct 31, 1999 this sequence version replaced gi:5686649.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved
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* 1 10988: contig of 10988 bp in length
* 10989 107771: gap of unknown length
* 107772 193020: contig of 96783 bp in length
* 193021 195835: gap of 85249 bp in length
* 195836 215387: contig of 2815 bp in length
* 195836 215387: gap of unknown length
* 195836 215387: contig of 19552 bp in length.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CIT-HSPC_28708"
BASE COUNT 74310 a 41080 c 38337 g 61386 t 274 others
ORIGIN
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Query Match 10.4%: Score 209.6; DB 42; Length 215387;
Best Local Similarity 63.2%: Pred. No. 7.7e-39;
Matches 373; Conservative 0; Mismatches 184; Indels 33; Gaps 2;

QY 1366 tatgacagacattgtatgaccaccacattgattcttctcaccgacttcacaag 1425
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Db 24631 TATGCGAGAGATGATTCATCCACAGCAATGATTCGCTTGATGACTTCACTG 24690
Oy 1426 tctcgaagaagatgagctgcttaccacaaccgtatgtaattgctggtgaccacaa 1485
Db 24691 TTGCGACGAAGATGGCGTATGACGAACCTGGTAGAATATGACCTGTAGAGAGATCAT 24750
Oy 1486 aaacataagctgctctgagggtagccaccaggttagcagtaattgcttggtagaacgt 1545
Db 24751 TACGAGCATTTCTCTGGAGATGACCTTAATAAGTCAACGAAAT----- 24793
Oy 1546 gcccaatacacacacaataatctcctgcatgagcaaaaaataataatgataataaata 1605
Db 24793 -----ACTCCTTTTCCAAAATGTCAAGAGAAGAAATATATGCGATATAAATG 24840
Oy 1606 tcaatataagaagaagttcgaaggtctgggcaaaaataatgaagaatttcaattgct 1665
Db 24841 TCAATTAGAGGAAGAAATCAACACTTTAGACGAAATATGAAAACTCTTCAAAATTTGCT 24900
Oy 1666 tgaagggttacaagaagctatgaaggtcgaagacaatttctgtaatttaccataaaga 1725
Db 1901 TGAAGGACTGCAAGAGACCTATGAAAGTCAAGAAATGATTTTGAATCCATCATCAAGGA 24950
Oy 1726 agcagcaaggttataaaaaagttgtcttaattcaagaactcgaagagcgcttaagaat 1785
Db 24961 AGCCACAGATTTATGAGACGAGACTTATTCAGCACCTTGAGAGAAACTGACAAAT 25020
Oy 1786 agatcccaactgcatctcgaagaaagttgaagacatgagaaataatggtttagt 1845
Db 25021 GATTCTGCGCTACTGTTCAAGAAAGATCATCTCACCCGAAATGCATATCTTGTAAATG 25080
Oy 1846 ---caagaaccgaaggaagaagaacatgctgtagatgagacaagttatcttctaa 1902
Db 25081 ACTGAGGAGGAAAAAGGCTCAATGCTGTTTCTAGAAATGAGCAGATATTTCTCTGA 25140
Oy 1903 gctccctaataatcctgaatgaagaagaatccctccgaagctcgaaga 1952
Db 25141 GCCTCTTGACATGCTTGTAGTAATAATGGCTTCAGAGGCTTAAGACA 25190

RESULT 3
LOCUS HS228P2T 476 bp DNA STS 29-OCT-1998
DEFINITION H sapiens STS from genomic clone 228P2, sequence tagged site.
ACCESSION AL032554
VERSION AL032554.1 GI:3810765
KEYWORDS STS: single read.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 476)
AUTHORS Ross, M., Dunham, A., Huckle, E., Taylor, R. and Hunt, S.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) E-mail contact: humquer@esanger.ac.uk
COMMENT Marker sts55154 (Primer A : TGGGATTTCTCCCGTGTGA; Primer B :
CACTTCTTCCCTCCACA; amplicon size : 175 bp) is from sequence
generated from the T7 end of PAC 228P2. 228P2 is part of the
bacterial clone contigs constructed by the Chromosome X Mapping
Group. (http://www.sanger.ac.uk/HGP/Chrx/) 228P2 is from the library
constructed at the Roswell Park Cancer Institute by the group of
Pieter de Jong.

For further details see <http://bacpac.med.buffalo.edu/>.
Location/Qualifiers
1. 476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="228P2"
BASE COUNT 129 a 99 c 109 g 139 t
ORIGIN

Query Match 5.9% Score 119.2: DB 13: Length 476;

Best Local Similarity 71.5% Pred. No. 8.2e-18:
Matches 173; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

Oy 1272 ctgtcatcagatatccagaagagagatgataatgataacccctctgtagtgc 1331
Db 241 CTGTCTATCATGAGGTCTATGTGGAGGGGAAAGAAAGTGTCAAAACCACTGATGCT 300
Oy 1332 tccgtcaattctgtagtaccagaagctgataaataatgacagagcatgtatgccacca 1391
Db 301 TTTACTCAAAATCTGTTTCACACAGAGT-----TATGACAGGACATGCTATTCACACCA 354
Oy 1392 atgcatgtagtcttctcctcagactcacaagctcgaagaagagagctgttaca 1451
Db 355 GCCAATTGATTTCTACAGTTATGATGCTTCTGTTTCAGCAAGATAGATGACGA 414
Oy 1452 aacctgataatgataattgctgtaggtagcaccacaaatacagtagtctctgcaagtacc 1511
Db 415 AACCTGTAGCAATGACACCTGTGGAGGAACGTTACACAGCATTTCTCTGAGATGACC 474
Oy 1512 ca 1513
Db 475 TA 476

RESULT 4
LOCUS HSM801162 1738 bp mRNA PRI 15-SEP-1999
DEFINITION Homo sapiens mRNA; CDNA DKFZp434B105 (from clone DKFZp434B105).
ACCESSION AL117626
VERSION AL117626.1 GI:5912207
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1738)
AUTHORS Diestereheft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) MIPS, Am Klopferplatz 18a D-82152
Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), sequenced by Qiagen within the CDNA
sequencing consortium of the German Genome Project. This clone is
available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
SOURCE

1. 1738
/organism="Homo sapiens"
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KQDEIDQVSPVLAQMGNYOYELKQVSPPLREDDPQPRRLATFGNPFKDKKGMID
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LOCUS CV089672 5726 bp DNA SYN 21-MAR-1997
 DEFINITION Cloning vector pIRES1hyg, complete plasmid sequence.
 ACCESSION U89672
 VERSION 089672.1 GI:1899166
 KEYWORDS bicistronic;
 SOURCE unidentified cloning vector.
 ORGANISM unidentified cloning vector.
 REFERENCE 1 (bases 1 to 5726)
 Rees, S., Coote, J., Stables, J., Goodson, S., Harris, S., and Lee, M.G.
 TITLE Bicistronic vector for the creation of stable mammalian cell lines
 that predispases all antibiotic-resistant cells to express
 recombinant protein
 JOURNAL Biotechniques 20 (1), 102-104 (1996)
 MEDLINE 96366236
 REFERENCE 2 (bases 1 to 5726)
 Lou, Y. and Holtz, A.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-1997) CLONTECH Laboratories, Inc., 1020 East
 Meadow Circle, Palo Alto, CA 94303-4230, USA
 This vector can be obtained from CLONTECH Laboratories, Inc., 1020
 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
 call (415) 424-8222 or (800) 662-2566, extension 1. International
 customers, please contact your local distributor. For technical
 information, call (415) 424-8222 or (800) 662-2566, extension 3.
 This sequence has been compiled from information in the sequence
 databases, published literature and other sources, together with
 partial sequences obtained by CLONTECH. If you suspect there is an
 error in this sequence, please contact CLONTECH's Technical Service
 Department at (415) 424-8222 or (800) 662-2566, extension 3 or
 E-mail TECH@CLONTECH.COM

FEATURES
 source Location/Qualifiers
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 HYHWQTVMDQTVASVVAQALDELMLAEDCEPVRHLVADEGSNNVLIDNGKITAVI
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 DRWPELNEAIPNDERDTTPVAMATTLRLRLTIGELLTASRQQLIDMEADVAPL
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BASE COUNT 1328 a 1482 c 1518 g 1398 t
 ORIGIN

Query Match 3.4%; Score 69; DB 14; Length 5726;
 Best Local Similarity 93.5%; Pred. No. 3.8e-06;
 Matches 72; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ctcaactaaggagaccacgcctgtgtaccagcctgcgacccagtagtaagccgcag 60
 DB 871 CTCACATATAGGAGACCAAGCTTGCTACCGAGCTCGATCCACTAGTAACGGCCGAC 930

QY 61 tgtctggaagtgtc 77
 DB 931 TGTCTGGAATTTATTC 947

RESULT 9
 LOCUS A49700 6802 bp DNA circular PAT 07-MAR-1997
 DEFINITION Sequence 6 from Patent WO9610641.
 ACCESSION A49700
 VERSION A49700.1 GI:2303036
 KEYWORDS
 SOURCE Influenza virus.
 ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 unclassified Orthomyxoviridae.
 REFERENCE 1 (bases 1 to 6802)
 Hobom, G., Neumann, G. and Menke, A.
 TITLE An attenuated vaccination virus, a method to make the virus and a
 pharmaceutical compositions comprising the virus
 JOURNAL Patent: WO 9610641-A 6 11-APR-1996;
 BAYER AG (DE)
 Other publication AU 3607695 960426.
 COMMENT
 FEATURES
 source Location/Qualifiers
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 /isolate="PHL1191"
 /db_xref="taxon:11309"

BASE COUNT 1674 a 1695 c 1742 g 1691 t
 ORIGIN

Query Match 3.4%; Score 68.4; DB 5; Length 6802;
 Best Local Similarity 98.6%; Pred. No. 5.3e-06;
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ctcaactaaggagaccacgcctgtgtaccagcctgcgacccagtagtaagccgcag 60
 DB 6697 CTCACATATAGGAGACCAAGCTTGCTACCGAGCTCGATCCACTAGTAACGGCCGAC 6756

QY 61 tgtctggaagtgtc 77
 DB 6757 TGTCTGGAATTTATTC 947

RESULT 10
 LOCUS A58521 10443 bp DNA circular PAT 05-MAR-1998
 DEFINITION Sequence 25 from Patent WO9638555.
 ACCESSION A58521
 VERSION A58521.1 GI:3714137
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 10443)
 Bogardt, T., Stringham, E. and Vandeckerckhove, J.
 TITLE PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH CONTROL CELL
 BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND PHARMACEUTICAL COMPOSITIONS
 CONTAINING THEM AND THEIR USE IN THE CONTROL OF CELL BEHAVIOUR
 JOURNAL Patent: WO 9638555-A 25 05-DEC-1996;
 BOGAERT THIERRY (BE)
 COMMENT Other publication AU 6123496 961218.
 FEATURES
 source Location/Qualifiers
 1..10443

BASE COUNT 2747 a 2731 c 2399 g 2566 t
ORIGIN

Query Match 3.4%: Score 68.4; DB 5; Length 10443;

Best Local Similarity 98.6%: Pred. No. 5.3e-06;

Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctccatagaggagaccagctgtgtaaccgagctcgagatccactagtaacgcccag 60
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Db 10349 CTCACATAGGAGACCAACCTTGTTACCGAGCTCGGATCCACTAGTACGCCGCCAG 10408

OY 61 ttgtctggaa 70
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Db 10409 TGTCTGGAA 10418

REFERENCE 11
EVE132038 3840 bp mRNA circular SYN 28-JUL-1999
DEFINITION Expression vector pCDPT.
ACCESSION AJ132038
VERSION AJ132038.1 GI:5640088
KEYWORDS AMP gene; beta lactamase; ColEI origin of replication; multiple cloning site; SP6 promoter; SV40 origin of replication; T7 promoter; xanthine-guanine phosphoribosyl transferase; xanthine-guanine phosphoribosyl transferase gene.
Expression vector pCDPT.
ORGANISM Expression vector pCDPT.
REFERENCE 1 (bases 1 to 3840)
AUTHORS Zeng,B.J.
TITLE Mammalian Expression Vector for with fuse Xanthine-guanine phosphoribosyl transferase Tag
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3840)
AUTHORS Zeng,B.J.
TITLE Direct Submision
JOURNAL Submitted (27-FEB-1999) Zeng B.J., Gene Engineering Center, Institute of Microbiology, Zhongguancun, Beijing, Beijing 100080, CHINA

SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3840)
AUTHORS Zeng,B.J.
TITLE Mammalian Expression Vector for with fuse Xanthine-guanine phosphoribosyl transferase Tag
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3840)
AUTHORS Zeng,B.J.
TITLE Direct Submision
JOURNAL Submitted (27-FEB-1999) Zeng B.J., Gene Engineering Center, Institute of Microbiology, Zhongguancun, Beijing, Beijing 100080, CHINA

FEATURES
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1. .3840
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209. .863
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864. .882
/note="T7"
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/product="Xanthine-guanine phosphoribosyl transferase"
/protein_id="XAB51567.1"
/db_xref="GI:5640089"
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/note="Multiple cloning site; HindIII, BamHI, BstXI, EcoRI, NotI, XhoI"
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/db_xref="GI:5640089"
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2644. .2729
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/db_xref="GI:5640090"
/translation="MSIOHFRVALIPEFFAACFLVFAHPETLVKVAEDQOLGARVY
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DRMPRELNEAIPNDERPTMPVAMATLRRLTGLGELLTLASROOLDIMPADVAGPL
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BASE COUNT 938 a 960 c 964 g 978 t
ORIGIN

Query Match 3.4%: Score 68.4; DB 14; Length 3840;
Best Local Similarity 98.6%: Pred. No. 5.3e-06;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctccatagaggagaccagctgtgtaaccgagctcgagatccactagtaacgcccag 60
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Db 796 CTCACATAGGAGACCAACCTTGTTACCGAGCTCGGATCCACTAGTACGCCGCCAG 855

OY 61 ttgtctggaa 70
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Db 856 TGTCTGGAA 865

RESULT 12
PCDNA3ZE0
LOCUS PCDNA3ZE0 3986 bp DNA SYN 16-AUG-1995
DEFINITION Cloning vector pCDNA3ZE0 DNA.
ACCESSION X90639
VERSION X90639.1 GI:949972
KEYWORDS cloning vector; expression vector; multiple cloning site; Plasmid.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 3986)
AUTHORS Peters,H., Hunderhausen,T., Kroenke,M. and Marget,M.
TITLE A new small sized high-level eukaryotic expression vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3986)
AUTHORS Peters,H.
TITLE Direct Submision
JOURNAL Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie, Michaelistr.5, D-24105 Kiel, FRG
COMMENT Related sequences: M21295 and K03104.
FEATURES
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1. .3986
/organism="synthetic construct"
/plasmid="pCDNA3ZE0"
/db_xref="taxon:32630"
1. .2125
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2126. .2796
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2797. .3986
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BASE COUNT 900 a 1057 c 1054 g 975 t
ORIGIN

Query Match 3.4%: Score 68.4; DB 14; Length 3986;
Best Local Similarity 98.6%: Pred. No. 5.3e-06;
Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ctccatagaggagaccagctgtgtaaccgagctcgagatccactagtaacgcccag 60
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Db 871 CTCACATAGGAGACCAACCTTGTTACCGAGCTCGGATCCACTAGTACGCCGCCAG 930

regulatory sequences

Db 1134 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 107

Oy 2008 aaaaaaa 2016
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Db 1074 RRRRRRRA 1066

Search completed: March 24, 2000, 04:11:30
Job time: 8624 sec